

Remarks

Reconsideration of this Application is respectfully requested.

The Examiner has indicated that the sequence disclosed in page 76, line 14 of the specification is not identified by a SEQ ID NO. (Office Communication, September 20, 2007). Applicants have amended herewith the specification at page 76, line 14, inserting the corresponding SEQ ID NO.

The Examiner has further indicated that, due to the poor quality of copy, the following pages of the specification contain sequences where the sequence or SEQ ID NO are illegible: 103, 104, 122-125, 127, 131-135, 137-140, 142-163, 165-176a, 177-183, 185, 187-189, 191-194, 198, 199, and 201-204. (Office Communication, September 20, 2007). Applicants have resubmitted herewith the above-cited pages with legible SEQ ID NOs.

Applicants respectfully request that the Examiner reconsider all outstanding objections and that they be withdrawn.

Applicants further respectfully request that the Examiner recommence substantive examination without further delay.

While Applicants note that the SEQ ID NO on page 76, line 14 is required under 37 C.F.R. §§ 1.821 through 1.825, Applicants' elected and claimed peptide has been clearly indicated in several responses to the United States Patent and Trademark Office, and the corresponding SEQ ID NO of Applicants' elected and claimed peptide has also been clearly indicated. (*See e.g.*, Reply to Restriction Requirement and Preliminary Amendment, filed March 26, 2002; Amendment and Reply to Restriction Requirement, filed October 16, 2002; Amendment and Reply, filed April 15, 2003; Amendment and

Reply, filed November 29, 2004; Amendment and Reply, filed August 29, 2005; Amendment and Reply, filed December 15, 2006). The correction to the specification at page 76, line 14, required in the current Office Communication does not impact the Examiner's ability to substantively examine Applicants' current application.

Additionally, with respect to pages 103, 104, 122-125, 127, 131-135, 137-140, 142-163, 165-176a, 177-183, 185, 187-189, 191-194, 198, 199, and 201-204, previously submitted to the USPTO on November 20, 2000, Applicants respectfully assert that the SEQ ID NOs of the pages in Applicants' file (which are hard copies of pages submitted to the USPTO) are legible.

Because Applicants understand that the quality of the scanned material on the USPTO's PAIR site varies (and perhaps was not of high quality in 2000 when the above-listed pages were originally submitted), Applicants have resubmitted the above-listed pages. However, Applicants assert that the pages that were previously submitted are legible. Furthermore, Applicants again assert that the elected and claimed sequence and SEQ ID NO have been clearly set forth previously in numerous responses and amendments, as set forth above, and that the replacement pages requested by the Examiner do no impact the Examiner's ability to substantively examine the current application.

Applicants also note the following statutory guidance:

Completeness of examiner's action. The examiner's action will be complete as to all matters, except that in appropriate circumstances, such as misjoinder of invention, fundamental defects in the application, and the like, the action of the examiner may be limited to such matters before further action is made. However, matters of form need not be raised by the examiner until a claim is found allowable.

37 C.F.R. § 1.104(b); *see also* MPEP 707.07.

Given that Applicants' elected peptide is recited in the above-listed Amendment and Replies, and the SEQ ID NO is clearly indicated, Applicants assert that the outstanding formalities issues raised in the current Office Action do not qualify as matter related to a fundamental defect in the application. Therefore, issuance of the outstanding Office Action raising only formalities requirements is not appropriate.

MPEP 707.07(a) provides further guidance related to formalities requirements. When outstanding formalities requirements are noted by the Office of Initial Patent Examination (OIPE) or by the Draftsperson, forms listing these requirements are placed in applications. *See* MPEP 707.07(a). Such forms are to be mailed to Applicants as a part of the examiner's first action:

In every instance where these forms are to be used, they should be mailed with the examiner's *first* action, and any additional formal requirements which the examiner desires to make should be included in the *first* action.

MPEP 707.07(a) (emphasis in original).

Applicants note that the current application was filed on July 19, 1999. During the course of prosecution of the current application, Applicants have responded on multiple occasions to requests to correct the sequence listing and/or the specification with regard to the formalities requirements. (*See* Transaction History of Appl. No. 09/357,757 (Exhibit B); *see also*, Amendment and Substitute Sequence Listing, filed April 30, 2001; Amendment and Reply, filed January 30, 2003; Amendment and Submission of Substitute Sequence Listing, filed January 20, 2004). Applicants have therefore responded to an initial action on formalities requirements, and have also

responded to two subsequent requests that were not presented in a "first action." These subsequent requests, in fact, were issued after examination of the application was well underway, resulting in a delay of examination.

Applicants note that raising all formalities requirements to correct the specification and/or the sequence listing at the same time, if possible, would greatly facilitate and expedite prosecution. When each correction is raised piecemeal, prosecution and examination of the application is delayed. This is neither cost-effective nor time-efficient for either the Examiner or Applicants.

Furthermore, when responses have been previously submitted regarding corrections to the specification and/or the sequence listing, Applicants have hoped that all of the Examiner's formalities concerns have been addressed. When a formalities request is issued in 2001, and then subsequently in 2002 and 2003, several years after the original application has been filed, particularly in the absence of any concomitant substantive examination, the examination of the application is seriously delayed.

The MPEP further states that:

Any application that has been pending for five years should be carefully studied by the supervisory patent examiner and every effort should be made to terminate its prosecution.

MPEP 707.02. Additionally, the MPEP notes that "piecemeal examination should be avoided as much as possible." MPEP 707.07(g).

Applicants have every desire to comply with the rules and put the specification in proper order. Applicants, however, hope that any future formalities concerns can be addressed in a way that will not further seriously delay prosecution of Applicants' current

application, especially in view of the fact that the current application has been pending since 1999.

In view of statutory guidance, the guidance in the MPEP, and the nature of the pending claims being examined, as discussed above, Applicants assert that any additional formalities requirements, if necessary, should be addressed once claims are found allowable.

Applicants further preserve the right, in view of the discussion above, to request appropriate patent term adjustment once claims have been found allowable.

Applicants respectfully request that the Examiner withdraw all objections and recommence substantive examination of the application.

Respectfully submitted,

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EXHIBIT

A

(Appl. No.: 09/357,737)

Table VII

HCV A01 Super Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101
ATGNLPCSF	1	165		10	13	93	
ATLFGAY	2	1265		8	14	100	
AVQWNRLLAF	3	1917		11	14	100	
CTGSSDLY	4	1128	1069.62	9	11	79	0.3700
CTRGVAKAVDF	5	1190		11	11	79	
CTWMNSTGF	6	555		9	11	79	
CVTQTVDF	7	1482		8	12	86	
DLEVTSTW	8	1657		9	12	86	
ETIMRSPVF	9	1207		9	12	86	
FSTYDTRCF	10	2670		8	11	79	
FTEAMTRY	11	2792		8	14	100	
FTGLTHIDAHF	12	1567		11	13	93	
GLPVOODHLEF	13	1552		11	12	86	
GLSAFSLHSY	14	2921	1073.03	10	11	79	0.0029
GLTHIDAHF	15	1569		9	13	93	
GSSYGFOY	16	2641		8	11	79	
GTFPINAY	17	2063		8	11	79	
GVAGALVAF	18	1863		9	12	86	
GVAKAVDF	19	1193		8	11	79	
GVLAALAAAY	20	1670	1174.19	9	12	86	
GVRVCEKAMLY	21	2619		11	14	100	
GVWLEDGWNV	22	154		11	12	86	
HLQNVNDVQY	23	696		11	11	79	
HMMNFSGIQY	24	1769		11	13	93	
HVGPGEGAVQW	25	1910		11	11	79	
IMAKNEVF	26	2591		8	12	86	
ITYSTYQKF	27	1296		9	12	86	
NDVQYLY	28	701		8	12	86	0.0130
KSTKVPAAY	29	1241	13.0016	9	12	86	
KVIDLTGCF	30	121		10	12	86	
LIEANLLW	31	2235		8	12	86	
LINTNGSW	32	414		8	11	79	
LLAPITAY	33	1030		8	14	100	
LLFNILGGW	34	1812		9	12	86	
LLSPRGSRPSW	35	97		11	11	79	0.8100
LSAFSLHSY	36	2922	13.0019	9	11	79	
LSPRGSRPSW	37	98		10	11	79	
LTOGFADLMGY	38	126		11	12	86	
LTHIDAHF	39	1570		8	13	93	
LVDILAGY	40	1853		8	11	79	
MILMTHFF	41	2876		8	12	86	
NNDVQYLY	42	700	1073.01	9	12	86	0.0980
NLPGCSFSIF	43	168		10	13	93	
NTCVTQTVDF	44	1460		10	12	86	
NTNRPPQDYKF	45	14		11	11	79	

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101
NVDDLVGW	46	1108		9	11	79	
PITYSTYKGF	47	1295		10	11	79	
PMGFSYDTRCF	48	2667		11	11	79	
PSVAATLGF	49	1261		9	14	100	
PTLHGPTPLLY	50	1621		11	11	79	
PVCOOHLEF	51	1554		9	12	86	
PVCOOHLEFW	52	1554		10	12	86	
QTVDFSLDPTF	53	1465		11	12	86	
RLHGLSAF	54	2918		8	12	86	
RLAPITAY	55	1029	1174.18	9	12	86	
RMAWDMMMNW	56	317		10	12	86	
RLMLMTHF	57	2875		8	12	86	
RLMLMTHFF	58	2875		9	12	86	
RVCCKWALY	59	2621	1174.21	9	14	100	
RVEEDGNY	60	156	1174.17	9	12	86	
STKVPAAV	61	1242		8	12	86	
SVAATLGF	62	1262		8	14	100	
SVAATLGFAY	63	1262		11	14	100	
TMAKNEVF	64	2590		9	11	79	
TLHGPTPLLY	65	1622	1073.04	10	11	79	0.0300
TLJFNILGW	66	1811		10	12	86	
TTIMAKNEVF	67	2589		10	11	79	
TTMFSPVF	68	1208		8	12	86	
TVDFSLDPTF	69	1466		10	12	86	
VIDLTGCF	70	122		9	12	86	
VLAALAAV	71	1671		8	12	86	
VLEDGNY	72	157		8	12	86	
VLVDILAGY	73	1852		9	11	79	
VMGSSYGF	74	2639		8	11	79	
VMGSSYGFQY	75	2639		10	11	79	
WMNRLUAF	76	1920		8	14	100	
YSPGQRNEF	77	2648		9	11	79	
YTNVDDLVGW	78	1106		11	11	79	
YVGDGQSVF	79	276		10	12	86	

Table X

HCV A24 Super Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
ALSPGAL	747	1850		8	13	93	
ALAHGVRVL	748	150	1013.16	9	14	100	
ALSTGLHL	749	689	1013.12	9	12	86	
ALVGVVCAAI	750	1896		11	11	79	
ATGNLPGCSF	751	165		10	13	93	
ATLFGAY	752	1265		8	14	100	
ATLFGAYM	753	1265		8	13	93	
AVAYYRGL	754	1419		8	14	100	
AVQWMNRL	755	1917		8	14	100	
AVQWMNRL	756	1917	1174.09	9	14	100	
AVQWMNRLJAF	757	1917		11	14	100	
AVQMMNRL	758	319		8	12	86	
AYAGGYKVL	759	1248	13.0132	10	11	79	0.0009
AYYRGLDYSVI	760	1421		11	14	100	
QLKLGVPPL	761	2941	1.0510	10	12	86	
CLNMMLLI	762	739		8	12	86	
CTGSSDL	763	1128		8	11	79	
CTGSSDL	764	1128		9	11	79	
CTGSSDL	765	1128	1069.62	10	11	79	
CTRGVAKAVDF	766	1190		11	11	79	0.0001
CTWMNSTGF	767	555		9	11	79	
CVTQTVDF	768	1462		8	12	86	
CVTQTVDFSL	769	1462	1.0487	10	12	86	
CYDAGCAW	770	1525		8	11	79	
CYDAGCAWY	771	1525	1.0125	9	11	79	
CYDAGCAWYEL	772	1525		11	11	79	
DFSLDPTF	773	1468		8	14	100	
DFSLDPTFI	774	1468		10	14	100	
DLCSSVPL	775	279		8	12	86	
DLEWITSTW	776	1657		9	12	86	
DLEWITSTWVL	777	1657		11	12	86	
DLGVRVCEKM	778	2617		10	13	93	
DLMGYPL	779	132		8	11	79	
DLNLLPAI	780	1883	14.0052	9	11	79	
DLNLLPAI	781	1883	1.0891	10	11	79	
DTAACGDI	782	994		8	12	86	
DTAACGDII	783	994		9	12	86	
DTLTCGFADL	784	124		10	12	86	
DTLTCGFADLM	785	124		11	12	86	
DKKFFGGGQI	786	21	1174.01	10	12	86	
DYPYRLWHY	787	615		9	14	100	
EPFYGKAI	788	1377	1174.07	9	13	93	
ETAGARLWL	789	1342		10	12	86	
ETIMRSPVF	790	1207		9	12	86	
EVTSTWVL	791	1659	1.0132	9	12	86	

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
FSGIQYL	792	1773		8	14	100	
FSGIQYLAGL	793	1773		11	14	100	
FLALLSCL	794	177	1.0818	9	12	86	
FTEAMTRY	795	2792		8	100	100	
FTGLTHIDAHF	796	1567		11	13	93	
FTLPALSTGL	797	684		11	11	79	
FWAKHMMNF	798	1765	24.0092	9	12	86	6.9000
FWAKHMMNFI	799	1765		10	12	86	
GFADLMGY	800	129		8	13	93	
GFADLMGYI	801	129		9	13	93	
GFADLMGYIPL	802	129		11	11	79	
GFSDYTRCF	803	2669		9	11	79	
GIQYLAGL	804	1776		8	14	100	
GIQYLAGLSTL	805	1776		11	14	100	
GLPVQDHL	806	1552	1.0126	9	13	93	
GLPVQDHLF	807	1552		11	12	86	
GLSAFSLSHY	808	2921	1073.03	10	11	79	0.0001
GLSTLPGNPAI	809	1782		11	11	79	
GLTHIDAHF	810	1569		9	13	93	
GLTHIDAHFL	811	1569	1.0488	10	13	93	
GTFPINAY	812	2063		8	11	79	
GVAGALVAF	813	1863		9	12	86	
GVAKAVDF	814	1193		8	11	79	
GVLAALAAAY	815	1670	1174.19	9	12	86	
GVLAALAAAYCL	816	1670		11	12	86	
GVNYATGNL	817	161	1.0099	9	11	79	
GVNVCEKM	818	2619		8	14	100	
GVNVCEKMAL	819	2619	1.0504	10	14	100	
GVNVCEKMALY	820	2619		11	14	100	
GVNLEDGVNY	821	154		11	12	86	
GVVCAAIL	822	1900		8	11	79	
GWRLAP1	823	1027		8	11	79	
GWRLAPITAY	824	1027		11	11	79	
GYGAGVAGAL	825	1859	13.0133	10	12	86	0.0003
GYPLVGAPL	826	135	13.0131	10	11	79	0.0057
GYRRCFASGL	827	2728		11	12	86	
HLQNVQVQY	828	696		11	11	79	
HLPYEQGM	829	1719		9	11	79	
HMMNFTSGI	830	1769	1174.08	9	13	93	
HMMNFTSGIQY	831	1769		11	13	93	
HTPVNSWL	832	2855		8	12	86	
HTPVNSWLGNI	833	2855		11	12	86	
HYGPGGAVQW	834	1910		11	11	79	
IFLLALLSCL	835	176		10	12	86	
ILGGWAAQL	836	1816	1090.16	10	12	86	0.0026

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
ILGIGTVL	837	1331		8	12	86	
IMAKNEVF	838	2591		8	12	86	
ITYSTYGKF	839	1296		9	12	86	
ITYSTYGKFL	840	1296		10	11	79	
INDVQVLY	841	701		8	12	86	
INGVYLL	842	30		8	13	93	
KFGGGGI	843	23		8	13	93	
KVIDLTGGE	844	121		10	12	86	
LVNLLGGW	845	1813		8	12	86	
UEANLLW	846	2235		8	12	86	
LNTNGSW	847	414		8	11	79	
LLALLSCL	848	178		8	12	86	
LLAPTAY	849	1030		8	14	100	
LLRNLLGW	850	1812		9	12	86	
LLPAILSPGAL	851	1887		11	13	93	
LLPRRGPRL	852	36	24.0066	9	13	93	
LLSPRGSRPSW	853	97		11	11	79	
LLWRGEMGGN	854	2240		11	12	86	
LTCGFADL	855	126		8	12	86	
LTCGFADLM	856	126		9	12	86	
LTCGFADLMGY	857	126		11	12	86	
LTHIDAHF	858	1570		8	13	93	
LTHIDAHFL	859	1570		9	13	93	
LTSMLTDPHSI	860	2176		11	13	93	
LTSOGNTL	861	2738		9	11	79	
LVDILAGY	862	1853		8	11	79	
LVGGVLAAL	863	1667		9	12	86	
LVNLFPSVAATL	864	1257	1.0133	11	14	100	
LVNLLPAI	865	1884		8	11	79	
LVNLLPAIL	866	1884	1.0825	9	11	79	
LVTRHADVI	867	1137	14.0048	9	11	79	
LVGVVCAAI	868	1897	40.0141	10	11	79	
LVGVVCAAIL	869	1897		11	11	79	
LWARMILM	870	2872		8	12	86	
LWARMILMTHF	871	2872		11	12	86	
LWRCBMGGN	872	2241		10	12	86	
LYLVTRHADVI	873	1135		11	11	79	
MILMTHFF	874	2876		8	12	86	
MLTDPHSI	875	2179		8	14	100	
MWNFSIGI	876	1770		8	14	100	
MWNFSIGIY	877	1770		10	14	100	
MWNFSIGIYLL	878	1770		11	14	100	
MYGGVGEHRL	879	636	1073.18	10	13	93	0.0270
NFSIGIY	880	1772		8	14	100	
NFSIGIYLL	881	1772	24.0091	9	14	100	0.0170

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
NILGGWVAQL	882	1815		11	12	86	
NIRTVGRIT	883	1282	1174.06	9	11	79	
NIVDVQYL	884	700		8	12	86	
NIVDVQYLY	885	700	1073.01	9	12	86	0.0001
NLGKVIDTL	886	118	939.18	9	12	86	
NLLWROEM	887	2239		8	12	86	
NLPGCSFSI	888	168	1174.02	9	13	93	
NLPGCSFSIF	889	168		10	13	93	
NLPGCSFSIFL	890	168		11	13	93	
NTCVTQTVDF	891	1460		10	12	86	
NTNGSWHI	892	416		8	13	93	
NTNRRPQDVKE	893	14		11	11	79	
NMODLVGW	894	1108		9	11	79	
NWFGTWM	895	551		8	12	86	
PITYSTYQKF	896	1295		10	11	79	
PITYSTYQKFL	897	1295		11	11	79	
PLEGPGDPL	898	2403		11	13	93	
PLGGAARAL	899	143	1.0093	9	11	79	
PMGFSYDTRCF	900	2667		11	11	79	
PTDPRRSRL	901	109		11	12	86	
PTLHGPTPL	902	1621		9	11	79	
PTLHGPTPL	903	1621		10	11	79	
PTLHGPTPLLY	904	1621		11	11	79	
PTLWARM	905	2870		8	11	79	
PTLWARMIL	906	2870		9	11	79	
PTLWARMILM	907	2870		10	11	79	
PTPLLYRL	908	1626		8	14	100	
PVODHLEF	909	1554		9	12	86	
PVODHLEFW	910	1554		10	12	86	
PVNSMLGNI	911	2857	1174.13	9	14	100	
PVNSMLGNI	912	2857	1174.14	10	14	100	
PVNSMLGNIM	913	2857		11	12	86	
PVHGOPL	914	2318		8	11	79	
QFKQKALGL	915	1732		10	12	86	
QFKQKALGL	916	1732		10	12	86	
QVGGVYL	917	29		8	13	93	
QVGGVYL	918	29	1.0088	9	13	93	
QVGGVYLL	919	1465		11	12	86	
QVDFSLDPTF	920	1919		9	14	100	
QWMNRLIAF	921	1778	13.0075	9	14	100	0.0480
QYLAGLSTL	922	2647	13.0134	10	11	79	0.0180
QYSPQQRVEF	923	2647		11	11	79	
QYSPQQRVEFL	924	2918		8	12	86	
RLHGLSAF	925	2918		10	11	79	
RLHGLSAFSL	926	2611	1090.21	8	11	79	0.0001
RLVFPDL							

HCV A24 Super Motif With Binding Information

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
TYSTYGKF	972	1297		8	13	93	
TYSTYGKFL	973	1297	13.0074	9	12	86	0.0230
VTGLTHI	974	1566		8	13	93	
VIDTLTCGF	975	122		9	12	86	
VLAALAAY	976	1671		10	12	86	
VLAALAAYCL	977	1671	1090.20	10	12	86	0.0070
VLEDGWY	978	157		8	12	86	
VLNPSVAATL	979	1258	1.0483	10	14	100	
VLTTSGNLT	980	2737	1.0505	10	11	79	
VLVDLAGY	981	1852		9	11	79	
VLGGVLAAL	982	1666	1.0492	10	12	86	
VMGSSYGF	983	2639		8	11	79	
VMGSSYGFQY	984	2639		10	11	79	
VTQTVDLSL	985	1463		9	12	86	
VTTHADVI	986	1138		8	11	79	
VVATDALM	987	1439		8	11	79	
VVGWVCAAI	988	1898		9	11	79	
VVGWVCAAIL	989	1898		10	11	79	
VTSTWVL	990	1660		8	12	86	
VYLPFRGPRIL	991	34	1073.19	11	13	93	0.0016
WMNRLJAF	992	1920		8	14	100	
WVLGGVL	993	1665		8	12	86	
WVLGGVLAAL	994	1665		11	12	86	
YIPLVGAPL	995	136	1.0817	9	11	79	
YLAGLSTL	996	1779		8	14	100	
YKSSGGPL	997	1165	1.0479	10	12	86	
YKSSGGGPL	998	1165		11	12	86	
YLPFRGPRIL	999	35	1073.07	10	13	93	0.0001
YLVTRHADVI	1000	1136		10	11	79	
YTNWQQQL	1001	1106		8	11	79	
YTNWQQDLGVW	1002	1106		11	11	79	
YWGLOGSVF	1003	276		10	12	86	
YWGLOGSVFL	1004	276		11	12	86	
YVGGVEHRL	1005	637	1.0107	9	13	93	
YYRGLDVSNI	1006	1422		10	14	100	

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
EKMALYDVV	1128	2624		9	12	86
FKQKALGL	1129	1733		9	12	86
GHRMAWDMM	1130	315		9	13	93
GKSTKVPAA	1131	1240		9	12	86
GRKPARLV	1132	2606		9	11	79
HRMAWDMM	1133	316		9	12	86
IKGGRHLF	1134	1390		9	11	79
KKKDELA	1135	1402		9	14	100
LHGLSAFSL	1136	2919		9	11	79
LHGPTLLY	1137	1623		9	11	79
LHSYSPGEI	1138	2927		9	11	79
LKSSGGPL	1139	1166		9	12	86
LRLGVPL	1140	2942		9	12	86
NHVSPTHYV	1141	1932		9	12	86
NRRPDVWF	1142	16		9	11	79
PRRGRLGV	1143	38		9	13	93
RHTPVNSWL	1144	2854		9	12	86
RHMVGFGEA	1145	1909		9	11	79
RKPARLVF	1146	2607		9	11	79
RRCRASGV	1147	2730		9	12	86
RPSNLGKV	1148	114		9	12	86
SKKKODELA	1149	1401		9	14	100
THVYPESDA	1150	1937		9	12	86
TKVPAAYAA	1151	1243		9	11	79
TRHADVIPV	1152	1139		9	11	79
TRVESENKV	1153	2251		9	12	86
VKFPGGGCI	1154	22		9	13	93
VRVCEKMAL	1155	2620		9	14	100
WRLAPITA	1156	1028		9	11	79
WRCBMGGN	1157	2242		9	12	86
YRGLDVSVI	1158	1423		9	13	93
YRRCRASGV	1159	2729		9	14	100
ARALAHGVRV	1160	148		10	13	93
ARAOAPPSPW	1161	1600		10	14	100
ARHTPVNSWL	1162	2853		10	11	79
ARMILMTHFF	1163	2874		10	11	79
CHSKKKODEL	1164	1399		10	12	86
DRDRSELSPL	1165	661		10	14	100
DRSELSPLL	1166	663		10	11	79
EKGGRKPARL	1167	2603		10	11	79
FRAAVCTRGV	1168	1185		10	11	79
GHRMAWDMM	1169	315		10	12	86
GKSTKVPAA	1170	1240	24.0096	10	12	86
GRKPARLVF	1171	2606		10	11	79
KHMMNFSGI	1172	1768		10	13	93

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
KKCDELAANKL	1173	1403		10	12	86
LHONIVDOY	1174	697		10	11	79
LKSSGGPRL	1175	1166		10	12	86
QKALGLLOTA	1176	1735		10	12	86
RMVGPGEAV	1177	1909		10	11	79
RRGPRLGVRA	1178	39		10	13	93
RRHVGPEGA	1179	1908		10	11	79
RRRSNLGKV	1180	113		10	12	86
RRSRNLGKVI	1181	114		10	12	86
SKFGYGAKDV	1182	2552		10	12	86
SKKKCELA	1183	1401		10	14	100
THYPESDAA	1184	1937		10	12	86
TRGVAKAVDF	1185	1191		10	11	79
TRVESENKV	1186	2251		10	12	86
VKFPGGQIV	1187	22		10	13	93
VRVCEKMAKY	1188	2620		10	14	100
VRVLEDGNY	1189	155		10	12	86
WILLAPITAY	1190	1028		10	11	79
YKVLVNPVS	1191	1254		10	14	100
YRRCRASGL	1192	2729		10	12	86
AHGVRLMDGV	1193	152		11	13	93
AKHMINFISGI	1194	1767		11	12	86
ARALAHGVRVL	1195	148		11	14	100
ARLVFPDLGV	1196	2610		11	11	79
CHSKKKCELA	1197	1399		11	14	100
DFRSELSPL	1198	661		11	11	79
EKGGRKPAPIL	1199	2603		11	11	79
FRAAVCTRGA	1200	1185		11	12	86
GKSTKVPAAVA	1201	1240		11	12	86
GKVIDTLTGSF	1202	120		11	12	86
HFMAWDMMMNW	1203	316		11	12	86
KKKCELAANKL	1204	1402		11	12	86
KRNTNRRPDV	1205	12		11	11	79
LHGPTLLYRL	1206	1623		11	11	79
LHONIVDOYL	1207	697		11	11	79
LKPTLHGPTPL	1208	1619		11	11	79
LRRHVGPEGA	1209	1907		11	13	93
PRRGPRLGVR	1210	38		11	12	86
PRRSNLGKV	1211	112		11	11	79
RRHVGPEGAV	1212	1908		11	11	79
RRRSNLGKVI	1213	113		11	12	86
SRGNHVSPTHY	1214	1929		11	12	86
SRNLGKVIDTL	1215	116		11	12	86
THYPESDAA	1216	1937		11	12	86
VRVLEDGWNVA	1217	155		11	12	86

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
YKVLNPSVA	1218	1254		11	14	100

Table XIII

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Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
AILRRHV	1219	1904		8	13	93
AALAAYCL	1220	1673		8	12	86
AAQGYKL	1221	1250		8	11	79
AATLGFGA	1222	1264		8	14	100
AAVCTRGV	1223	1187		8	12	86
ASLMFTA	1224	1793		8	11	79
ASSASQL	1225	2204		8	14	100
ATLGFAY	1226	1265		8	14	100
CSFSRL	1227	172		8	14	100
CSGGAYDI	1228	1310		8	12	86
CSSNVSA	1229	2819		8	14	100
CTOSSDL	1230	1128		8	11	79
CTRGVAKA	1231	1190		8	11	79
DTAACGDI	1232	994		8	12	86
DTLTGFA	1233	124		8	12	86
EALLENLV	1234	750		8	11	79
EAITRYSA	1235	2794		8	14	100
ESDAARV	1236	1942		8	12	86
ETAGARLV	1237	1342		8	12	86
ETIMRSPV	1238	1207		8	12	86
FADLMGYI	1239	130		8	13	93
FASRGHIV	1240	1927		8	14	100
FSIFLLAL	1241	174		8	14	100
FSYDTRCF	1242	2670		8	11	79
FTEAMTRY	1243	2792		8	14	100
FTSPVW	1244	512		8	13	93
GAGVAGAL	1245	1861		8	12	86
GAHWGVLA	1246	350		8	12	86
GALVGVW	1247	1895		8	11	79
GARLVLA	1248	1345		8	12	86
GSQKSTKV	1249	1238		8	13	93
GSSDLV	1250	1131		8	12	86
GSSGGPLL	1251	1168		8	12	86
GSSYGFOY	1252	2641		8	11	79
GTFPINAY	1253	2063		8	11	79
HSYSPGEI	1254	2928		8	11	79
HTPNSWL	1255	2855		8	12	86
ISGIOYLA	1256	1774		8	14	100
ITSCSSW	1257	2816		8	14	100
ITWGAOTFA	1258	989		8	12	86
KSTKVPA	1259	1241		8	12	86
LAVGAGV	1260	1857		8	11	79
LAHGVRL	1261	151		8	14	100
LAVAVEPV	1262	972		8	11	79
LSAPSLKA	1263	2211		8	11	79

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
LSFGALVV	1264	1892		8	13	93
LSTGLIHL	1265	690		8	12	86
LTOGFADL	1266	126		8	12	86
LTHIDAHF	1267	1570		8	13	93
MSADLEW	1268	1654		8	11	79
NSWLGNII	1269	2859		8	14	100
NTCVGTIV	1270	1460		8	12	86
NTNGSWHI	1271	416		8	13	93
PAILSPGA	1272	1889		8	13	93
PALSTGLI	1273	688		8	12	86
PTLWARMII	1274	2870		8	11	79
PTPLLYRL	1275	1626		8	14	100
OATVCARA	1276	1595		8	13	93
RAPPRWFM	1277	3019		8	14	100
RSELSPLL	1278	664		8	11	79
RSRNLGKV	1279	115		8	12	86
SFSLHSY	1280	2923		8	11	79
SSASQLSA	1281	2206		8	14	100
STKVPAAAY	1282	1242		8	12	86
STLPGNPA	1283	1784		8	14	100
STLPQAVM	1284	2633		8	12	86
STYGFELA	1285	1299		8	12	86
TAACGDII	1286	995		8	12	86
TAGARLW	1287	1343		8	12	86
TTMRSPVF	1288	1208		8	12	86
TTSCGNIL	1289	2739		8	11	79
VAGALVAF	1290	1864		8	12	86
VTRHADVI	1291	1138		8	11	79
VTSTWVLV	1292	1661		8	12	86
WAKHMMNF	1293	1766		8	14	100
WAKYLVIM	1294	368		8	12	86
WACFGYPW	1295	76		8	12	86
YAAQGYKV	1296	1249		8	11	79
YSIEPLDL	1297	2905		8	11	79
YSTYGKFL	1298	1298		8	12	86
YTWDDDL	1299	1106		8	11	79
AAKLODCTM	1300	2758		9	16	114
AAQGYKVLV	1301	1250		9	11	79
AARALAHGV	1302	147		9	11	79
AATLFGGAY	1303	1264		9	14	100
AAVCTRGA	1304	1187		9	11	79
ASQLSAPSL	1305	2208		9	13	93
ATLFGGAYM	1306	1265		9	26	186
ATVCARAQA	1307	1596		9	11	79
CAAILRRHV	1308	1903		9	13	93

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
QAEIAGARL	1354	1340		9	12	86
RAAVCTRGV	1355	1186		9	12	86
RAAHGVRV	1356	149	24.0063	9	14	100
RAQAPPPSW	1357	1601		9	11	79
HAYAMDRM	1358	811		9	16	114
RSELSPLL	1359	664		9	11	79
RSRNLGKI	1360	115		9	12	86
SSASQSLA	1361	2205		9	14	100
STKVPAAVA	1362	1242		9	12	86
STLPGNPAL	1363	1784	40.0083	9	11	79
STWLVGGV	1364	1663		9	12	86
TAGARLVVL	1365	1343		9	12	86
TSCSSNSV	1366	2817		9	14	100
TTIMAKNEV	1367	2589		9	11	79
VAATLGFGA	1368	1263		9	14	100
VAGGHVQM	1369	933		9	14	100
VAYQATVCA	1370	1592	40.0071	9	12	86
VAYYRGLDV	1371	1420	24.0064	9	14	100
VSTLPQAVM	1372	2632		9	12	86
VTQTVDFSL	1373	1463		9	12	86
WAKHMMNF	1374	1766	24.0070	9	12	86
YAAQGYKVL	1375	1249		9	11	79
YAPTLWARM	1376	2668		9	14	100
YSPGEINRV	1377	2930		9	11	79
YSPGQRFV	1378	2648		9	11	79
YSTYQKFLA	1379	1298		9	12	86
YTNWDDLV	1380	1106		9	11	79
AAQGYKVLVL	1381	1250		10	11	79
AATLFGAYM	1382	1264		10	26	186
ASLRVFTFAM	1383	2787		10	12	86
ASSASQSLA	1384	2204		10	14	100
ATGNLPGCSF	1385	165		10	13	93
CSFSIFLLAL	1386	172		10	14	100
CTCGSSDLYL	1387	1128		10	11	79
DARYCACLWM	1388	733		10	11	79
DSVIDONTCV	1389	1454		10	18	129
DTLTGCFADL	1390	124		10	12	86
ENLLWFRDM	1391	2237		10	24	171
ETAGARLVWL	1392	1342		10	12	86
FADLMGYIPL	1393	130		10	11	79
FTEAMTRYSA	1394	2792		10	14	100
GAARALAHGV	1395	146		10	11	79
GADTAACGDI	1396	992		10	11	79
GAGVAGALVA	1397	1861		10	12	86
GALWGVNCA	1398	1895		10	11	79

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
GARLVVLATA	1399	1345		10	11	79
GAVQVMNRLL	1400	1916		10	14	100
GGGKSTKVP	1401	1238		10	12	86
GTVLDOAETA	1402	1335		10	14	100
HSKKKDELA	1403	1400		10	14	100
IAFASRGNHV	1404	1925		10	14	100
ISGIOYLAGL	1405	1774		10	14	100
ITRVESENKV	1406	2250		10	12	86
ITSCSNVSV	1407	2816		10	14	100
ITYTYGKFL	1408	1296		10	11	79
KSTKVPAAAYA	1409	1241		10	12	86
LADGGSCGA	1410	1305		10	11	79
LAQFRKQKAL	1411	1729		10	12	86
LALPPRAYAM	1412	806		10	12	86
LSFGALVVG	1413	1892		10	13	93
LSPRGSRPSW	1414	98		10	11	79
LSRAPRWFM	1415	3017		10	14	100
LSTLPGNPAL	1416	1783		10	11	79
LTHPTKYIM	1417	1642		10	16	114
NTCVTQTVDF	1418	1460		10	12	86
PALSPGALV	1419	1889		10	12	86
PALSTGLJHL	1420	688		10	12	86
PARLIVFPDL	1421	2609		10	11	79
PSWDMWKCL	1422	1607		10	11	79
PTSGGKSTKV	1423	1236		10	13	93
PTHYVPESDA	1424	1936		10	12	86
PTLHGPTPL	1425	1621		10	11	79
PTLWARMILM	1426	2870		10	22	157
PTPLLYRLGA	1427	1626		10	13	93
QAEIAGARLV	1428	1340		10	12	86
QAPPPSWDDM	1429	1603		10	24	171
QATVCARAOA	1430	1595		10	11	79
RAAKLODCTM	1431	2757		10	16	114
RAAVCTRGVA	1432	1186		10	11	79
RALAHGVRVL	1433	149		10	14	100
SASOLSAPSL	1434	2207		10	13	93
STKVPAAYAA	1435	1242		10	11	79
STWLVGGVL	1436	1663		10	12	86
TAGARLVILA	1437	1343		10	12	86
TARHTPVNSW	1438	2852		10	11	79
TSCSNVSVSA	1439	2817		10	14	100
TSMLTDPHSI	1440	2177		10	13	93
TSTWLVGGV	1441	1662		10	12	86
TTIMAKNEVF	1442	2589		10	11	79
TTLPALSTGL	1443	685		10	11	79

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
VAATLGFAY	1444	1263		10	14	100
VTPGERPSGM	1445	1507		10	16	114
VTRHADVIPV	1446	1138		10	11	79
WAQPGYPWPL	1447	76		10	12	86
WAFMILMTHF	1448	2873		10	12	86
WAPDYNPPL	1449	2297		10	11	79
YAAQGYKVLV	1450	1249		10	11	79
YSPGENRVA	1451	2930		10	11	79
YSPGQRMERL	1452	2648		10	11	79
YSPGQRMERL	1453	147		11	11	79
AARALAHGVRV	1454	2786		11	12	86
AASLRVFTFAM	1455	1187		11	11	79
AAVCTRGVAKA	1456	1717		11	14	100
ASHLPYEQGM	1457	2208		11	11	79
ASOLSAFSLKA	1458	1599		11	11	79
CARQAAPPSPW	1459	172		11	14	100
CSFSIFLLALL	1460	1128		11	11	79
CTGSSSOLYL	1461	1190		11	11	79
CTRGVAKAVDF	1462	733		11	16	114
DARVCACLWMNM	1463	124		11	24	171
DTLTGCFADLM	1464	1342		11	12	86
ETAGARLVILA	1465	130		11	11	79
FADLMGYPLV	1466	2925		11	11	79
FSLSHSYSGEI	1467	1567		11	13	93
FTGLTHIDAHF	1468	684		11	11	79
FTLTPALSTGL	1469	992		11	12	86
GADTAACGDII	1470	1861		11	12	86
GAGVAGALVAF	1471	1895		11	11	79
GALVVGVVCAA	1472	1916		11	14	100
GAVQWMNRLIA	1473	1238		11	12	86
GSQKSTKVPAA	1474	1400		11	14	100
HSKXKCDLAA	1475	2928		11	11	79
HSYSPGENRV	1476	2855		11	12	86
HTPVNSWLGNI	1477	2250		11	14	100
ITRVESNKVV	1478	2816		11	14	100
ITSCSNVSVVA	1479	1296		11	11	79
ITYSTYKFLA	1480	1241		11	11	79
KSTKVPAAAYAA	1481	1305		11	11	79
LADGGCGGGAY	1482	1857		11	11	79
LAGYGAGVAGA	1483	2479		11	14	100
LSNSLRHHNM	1484	1892		11	11	79
LSPGALVGVW	1485	126		11	11	86
LTCGFADLMGY	1486	2176		11	13	93
LTSMLTDPHSI	1487	1418		11	13	93
NAVAYYRGLDV	1488	14		11	11	79
NTNRRPDQVKF						

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
PAILSPGALVV	1489	1889		11	12	86
PSVAATLGFGA	1490	1261		11	14	100
PTDPRRSRNL	1491	109		11	12	86
PHYYPESDAA	1492	1936		11	12	86
PTLHGPTPLY	1493	1621		11	11	79
PTPLYLRLGAV	1494	1626		11	13	93
QAEAGARLVV	1495	1340		11	12	86
QAPPSWDQIMW	1496	1603		11	11	79
QIVDFSLDPTF	1497	1465		11	12	86
RSQPRGRCPPI	1498	55		11	13	93
SADLEVVTSTW	1499	1655		11	11	79
SSASQLSAPSL	1500	2206		11	13	93
SSDLYLVTRHA	1501	1132		11	12	86
STWLVGGVLA	1502	1663		11	12	86
TARHTPVNSWL	1503	2852		11	11	79
TSLTGRDKNOV	1504	1050		11	12	86
TSTWLVGGVL	1505	1662		11	12	86
TTLPALSTGLJ	1506	685		11	11	79
VAATLGFQAYM	1507	1263		11	26	186
VAGALVAFKVM	1508	1864		11	14	100
VAVEPWFFSDM	1509	974		11	12	86
VAYQATVCARA	1510	1592		11	11	79
VAYYRGLDVSV	1511	1420		11	14	100
VTSTWLVGGV	1512	1661		11	12	86
WAQFGYPWPLY	1513	76		11	12	86
WARMILMTHFF	1514	2873		11	12	86
YAAQGYKVLVL	1515	1249		11	11	79
YATGNLPGCSF	1516	164		11	12	86
YTNVDDQLVGW	1517	1106		11	11	79

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
KMALYDVV	1563	2625	29.0037	8	12	86
KPARLIVF	1564	2608		8	12	86
KOKALGLL	1565	1734		8	12	86
KVPAAYAA	1566	1244		8	11	79
UEANLLW	1567	2235	29.0038	8	12	86
LINTNGSW	1568	414		8	11	79
LLALLSCL	1569	178		8	12	86
LLAPITAY	1570	1030		8	14	100
LLADARV	1571	729	29.0039	8	13	93
LLYRLGAV	1572	1629		8	13	93
LMGYIFLV	1573	133		8	11	79
LPALSTGL	1574	687		8	14	100
LPGCSFSI	1575	169	29.0040	8	13	93
LPRRGPRL	1576	37		8	13	93
LPVODDHL	1577	1553		8	13	93
LPVIEOGM	1578	1720		8	12	86
LODCTMLV	1579	2761	29.0041	8	12	86
LVAYOATV	1580	1591		8	12	86
LVDLAGY	1581	1853		8	11	79
LVGGMLAA	1582	1667		8	12	86
LVLNPSVA	1583	1257	29.0042	8	14	100
LVNLLPAI	1584	1884		8	14	100
LVTRHADV	1585	1137		8	11	79
LVGWVCA	1586	1897		8	12	86
LVICESA	1587	2773	29.0043	8	11	79
MILMTHFF	1588	2876		8	11	79
MLTDPShI	1589	2179		8	12	86
NILGGIWA	1590	1815		8	14	100
NIVDVQYL	1591	700	29.0044	8	12	86
NLLWRCBM	1592	2239		8	12	86
NPSVAATL	1593	1260		8	12	86
PLGGAARA	1594	143		8	14	100
PLLYRLGA	1595	1628	29.0045	8	11	79
PPPSWDQM	1596	1605		8	13	93
PPSWDQMW	1597	1606		8	12	86
PWHGGPFL	1598	2318		8	11	79
QNGGMYL	1599	29	29.0046	8	13	93
QLLRIPA	1600	336		8	13	93
QFETDLEL	1601	2808		8	12	86
QPGYFWPL	1602	78		8	11	79
RLHGLSAF	1603	2918	29.0047	8	12	86
RLVFPDL	1604	2611		8	12	86
RLAPITA	1605	1029		8	11	79
RLVLATA	1606	1347		8	12	86
RMAWDMMM	1607	317		8	12	86

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
RMILMTHF	1608	2875		8	12	86
RPDYNPPL	1609	2299	29.0048	8	11	79
ROBMGNI	1610	2243		8	12	86
RVCEKML	1611	2621		8	14	100
RVESENKV	1612	2252		8	12	86
RVGDHVV	1613	2100		8	11	79
SIFLLALL	1614	175		8	14	100
SIDPTFTI	1615	1470		8	14	100
SPGENRV	1616	2931	29.0049	8	11	79
SPGORVEF	1617	2649	29.0050	8	11	79
SQLSAPSL	1618	2209		8	13	93
SVAATLGF	1619	1262		8	14	100
TIMAKNEV	1620	2590		8	11	79
TLGFGAYM	1621	1266		8	13	93
TLHGPTPL	1622	1622		8	11	79
TLPGNPPI	1623	1785		8	11	79
TLWARMIL	1624	2871		8	11	79
TPCSGSWL	1625	1975	29.0051	8	12	86
TPGCYPCV	1626	223	29.0052	8	12	86
TGTVDPSL	1627	1464		8	12	86
TVCARAQA	1628	1597		8	11	79
VIDQNTCV	1629	1456		8	12	86
VLAALAAV	1630	1671		8	12	86
VLECYDA	1631	1521		8	13	93
VLDQAETA	1632	1337		8	14	100
VLNPSVAA	1633	157		8	12	86
VLNPSVAA	1634	1258		8	14	100
VLVGGVLA	1635	1666		8	12	86
VLVLPSPV	1636	1256		8	14	100
VMGSSYGF	1637	2639		8	11	79
VPESDAAA	1638	1940	29.0053	8	12	86
VQMMNRLI	1639	1918		8	14	100
VVATDALM	1640	1439		8	11	79
VGVVCAAA	1641	1898		8	11	79
VVTSTWVL	1642	1660		8	12	86
WMNRLJAF	1643	1920		8	14	100
WPLILLLL	1644	799	29.0054	8	12	86
WLVGGM	1645	1665		8	12	86
YLAGLSL	1646	1779		8	14	100
YFRLWHY	1647	616	29.0055	8	14	100
YVPESDAA	1648	1939		8	12	86
AILSPGALV	1649	1890	24.0067	9	12	86
ALAHGVRVL	1650	150	1.0094	9	14	100
ALSTGLIHL	1651	689	1.0109	9	12	86
ALVVGWVCA	1652	1896	40.0089	9	11	79

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
APPSWDQM	1653	1604	15.0051	9	12	86
APTLWARIMI	1654	2869	15.0063	9	11	79
ACGYKVLVL	1655	1251		9	11	79
ACGYGPWPL	1656	77		9	12	86
AVQWNNRLI	1657	1917	1174.09	9	14	100
KMSADLEW	1658	1653	1.0131	9	11	79
DLOGSVFLV	1659	279	1.0101	9	11	79
DLEVTSTW	1660	1657		9	12	86
DLMGYIPLV	1661	132	1.0816	9	11	79
DLVLLPAI	1662	1883	14.0052	9	11	79
DLWCESA	1663	2772		9	11	79
DLVLVTRHA	1664	1134	24.0074	9	12	86
DPQLSDGSW	1665	2410	15.0058	9	11	79
DPFRFSRNL	1666	111	15.0043	9	12	86
EPFYGKAI	1667	1377	1174.07	9	13	93
EMSGNITRV	1668	2245	1174.11	9	12	86
EWTSTWVL	1669	1659	1.0132	9	12	86
FISGIQYLA	1670	1773	40.0082	9	14	100
FLALLSCL	1671	177	1.0818	9	12	86
FLLLADARV	1672	728	1.0113	9	13	93
FQYSPGQGV	1673	2646		9	11	79
GIGTLDQA	1674	1333	1.0126	9	14	100
GLPVQDHL	1675	1552	1.0114	9	13	93
GLRLAVAV	1676	968		9	11	79
GLTHDAHF	1677	1569		9	13	93
GPGEAGQW	1678	1912	15.0055	9	12	86
GPTPLLYRL	1679	1625	15.0053	9	14	100
GQVGGVYL	1680	28		9	13	93
GVAGALVAF	1681	1863		9	12	86
GVLAALAA	1682	1670	1.0134	9	12	86
GVNYATGNL	1683	161	1.0099	9	11	79
GVRVCEKWA	1684	2619		9	14	100
GVRLEDGV	1685	154	1.0095	9	13	93
HLHQINVDV	1686	696	1.0111	9	12	86
HLPIECGM	1687	1719		9	11	79
HMMNFRSGI	1688	1769	1174.08	9	13	93
HQNVIVQY	1689	698		9	11	79
HVGPEGAV	1690	1910		9	11	79
ILAGYGAGV	1691	1856	1.0135	9	11	79
ILSPGALV	1692	1891	24.0065	9	13	93
KVLVLNPSV	1693	1255	1174.05	9	14	100
LITSCSNV	1694	2815	1.0147	9	14	100
LVRPDLGV	1695	2612	1.0826	9	11	79
LLFLLADA	1696	726	24.0071	9	14	100
LLNLLGGW	1697	1812		9	12	86

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
LLPRRGRL	1698	36	24.0066	9	13	93
LPAILSPGA	1699	1888	16.0013	9	13	93
LPALSTGLI	1700	687	15.0048	9	12	86
LPCEPEFDV	1701	2165	15.0056	9	12	86
LPQCSFSIF	1702	169	15.0044	9	13	93
LVGGVLAAL	1703	1667	1.0133	9	12	86
LVNPSVAA	1704	1257	1.0825	9	14	100
LVNLLPAIL	1705	1884	14.0048	9	11	79
LVTRHADVI	1706	1137		9	11	79
LVGWVCAA	1707	1897		9	11	79
NILGGWVAA	1708	1815		9	12	86
NIRTGVRTI	1709	1282	1174.06	9	11	79
NIVDVQVLY	1710	700	1.0112	9	12	86
NILGKVIDTL	1711	118	1.0091	9	12	86
NLPQCSFSI	1712	168	1174.02	9	13	93
NWDDLGVW	1713	1108		9	11	79
PLGGAARAL	1714	143	1.0093	9	11	79
PLLYRLGAV	1715	1628	1.0130	9	13	93
PPPSWQDMW	1716	1605	15.0052	9	11	79
PPWHGGFL	1717	2317	29.0070	9	11	79
POPEVDLEI	1718	2807		9	11	79
PVOOCHLEF	1719	1554		9	12	86
PVNSWLGNI	1720	2857	1174.13	9	14	100
QINGGVYLL	1721	29	1.0088	9	13	93
QLSAPSLKA	1722	2210		9	11	79
QPEYDLEI	1723	2808	15.0062	9	11	79
QFGYWPPLY	1724	78	15.0040	9	12	86
QPRGRRCPI	1725	57	15.0039	9	13	93
RLAPITAY	1726	1029	1.0116	9	12	86
RMILMTHFF	1727	2875		9	12	86
RVCEKMALY	1728	2621	1.0145	9	14	100
RVESENKVV	1729	2252	1.0138	9	12	86
RVLGDVNY	1730	156	1.0096	9	12	86
SMLTDPFSI	1731	2178	1174.10	9	14	100
SFGALVGVV	1732	1893	15.0054	9	13	93
SPGEINRVA	1733	2931	16.0015	9	11	79
SPQQRMEEL	1734	2649	15.0060	9	11	79
SPRGRSPSW	1735	99	15.0042	9	11	79
SVIDONTCV	1736	1455	1.0124	9	12	86
TIMAKNEVF	1737	2590		9	11	79
TLHGPTPLL	1738	1622	1.0129	9	11	79
TLPALSTGL	1739	686	1.0108	9	11	79
TLTGCFADL	1740	125	1.0092	9	12	86
TLWARMILM	1741	2871		9	11	79
TPLLYRLGA	1742	1627	16.0017	9	13	93

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
TVLDOAETA	1743	1336		9	14	100
VIDILTQGF	1744	122		9	12	86
VLEDGNYA	1745	157		9	12	86
VLVDILAGY	1746	1852		9	11	79
VLVGGVJAA	1747	1666	24.0075	9	12	86
VLVLNPSVA	1748	1256	24.0072	9	14	100
VQMMNRJIA	1749	1918		9	14	100
VVGWVCAAI	1750	1898		9	11	79
VTSTWLV	1751	1680	1.0823	9	12	86
WMNRLAFA	1752	1920	24.0073	9	14	100
WVLVGGVLA	1753	1665	40.0075	9	12	86
YIPLVGAPL	1754	136	1.0817	9	11	79
YLVAYQATV	1755	1590	1.0127	9	12	86
YLVTRHADV	1756	1136	1.0119	9	12	86
YQATVCARA	1757	1594		9	13	93
YVGDQSSV	1758	276	1.0100	9	12	86
YVGGVBHRL	1759	637	1.0107	9	13	93
YVPESDAAA	1760	1939		9	12	86
AILSPGALV	1761	1890	24.0101	10	12	86
ALVVGWVCAA	1762	1896		10	11	79
APPSWDQMM	1763	1604	15.0233	10	11	79
APTLWARML	1764	2869	15.0247	10	11	79
AQGYTPWPLY	1765	77		10	12	86
AVGYRGLDV	1766	1419	1.0486	10	14	100
AVCTRGVAKA	1767	1188		10	11	79
AVQMMNRJIA	1768	1917		10	14	100
CLRLGVPL	1769	2941	1.0510	10	12	86
CVTQVDFSL	1770	1462	1.0487	10	12	86
DILAGYGAGV	1771	1855	1.0495	10	11	79
DLEWVTSWV	1772	1657	1.0490	10	12	86
DLGVRVCEKM	1773	2617		10	13	93
DLSDGSWSTV	1774	2412	1.0499	10	11	79
DLVNLIPAIL	1775	1883	1.0891	10	11	79
DOAETAGARL	1776	1339		10	12	86
DMKFRGGGQI	1777	21	1174.01	10	12	86
ELTSCSSNV	1778	2814	1.0506	10	14	100
EQRKQKALG	1779	1731		10	12	86
EWVTSWLV	1780	1659	1.0491	10	12	86
GLSARLSHSY	1781	2921	1.0509	10	11	79
GLSTLPGNPA	1782	1782		10	14	100
GLTHDAHFL	1783	1569	1.0488	10	13	93
GPREGAVQMM	1784	1912	15.0240	10	12	86
GGVGGVYLL	1785	28		10	13	93
GVCWTVYHGA	1786	1081		10	11	79
GVRCERKVAL	1787	2619	1.0504	10	14	100

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
HONIVDOYL	1788	698		10	11	79
ILAGYGAGVA	1789	1856	40.0140	10	11	79
ILGGWVAQL	1790	1816	1.0493	10	12	86
IMAKNEFCV	1791	2591	1.0500	10	11	79
IQYLAGLSTL	1792	1777		10	14	100
IVFDLGVRV	1793	2613	1.0503	10	11	79
KPTLHGPTPL	1794	1620	15.0234	10	11	79
KVIDLTGCF	1795	121		10	12	86
KVLVLPNSVA	1796	1255		10	14	100
LLRNILGGW	1797	1812	1.0890	10	12	86
LLPAILSPGA	1798	1887	24.0102	10	13	93
LMGYPLVGA	1799	133		10	11	79
LPAILSPGAL	1800	1888		10	13	93
LPGCSFSIFL	1801	169	15.0238	10	13	93
LPRRGPRLGV	1802	37	15.0220	10	13	93
LPVODHLEF	1803	1553	15.0218	10	13	93
LVAYQATVCA	1804	1591	15.0232	10	12	86
LVDLIAGYGA	1805	1853	40.0133	10	11	79
LVGGVLAALA	1806	1667	40.0139	10	12	86
LWGWCAAI	1807	1897		10	11	86
MLTDPSHITA	1808	2179	40.0141	10	11	79
NLPGCSFSIF	1809	168		10	13	100
NPSVAATLGF	1810	1260	15.0230	10	14	100
PITYSTYKGF	1811	1295		10	11	79
PLGGAARALA	1812	143		10	11	79
POPEYOLEI	1813	2807		10	11	79
PVODHLEFW	1814	1554		10	12	86
PVNSWLGNI	1815	2857	1174.14	10	14	100
PVYCTFSPV	1816	508	1.0471	10	13	93
QLPDEPFDV	1817	2164	1.0497	10	12	86
OFPEKGRKPA	1818	2601	16.0188	10	11	79
RLHGLSAFSL	1819	2918	1.0508	10	11	79
RLVFPDLGV	1820	2611	1.0502	10	11	79
RMADWMMINW	1821	317		10	12	86
RVLEDGVNYA	1822	156		10	12	86
SLHSYSPGEI	1823	2926	1174.15	10	11	79
SLTGRDKNQV	1824	1051	1.0478	10	12	86
SPGALVWGW	1825	1893	15.0239	10	11	79
SOLSAFSLKA	1826	2209		10	11	79
SOPRGRROP	1827	56		10	13	93
SVAATLGFGA	1828	1262		10	14	100
TLHGPTPLLY	1829	1622	1.0489	10	11	79
TLRNILGGW	1830	1811		10	12	86
TLPALSTGLI	1831	686	1174.03	10	11	79
TLTCGFADLM	1832	125		10	12	86

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
TPCTGSSDL	1833	1126	15.0228	10	11	79
TPLLYRLGAV	1834	1627	15.0235	10	13	93
TPVNSMLGNI	1835	2856	15.0246	10	12	86
TVDFSLDPTF	1836	1466		10	12	86
VIDLTG3FA	1837	122		10	12	86
VLAALAAAYCL	1838	1671	1.0889	10	12	86
VLDQAEATGA	1839	1337		10	12	86
VLNPSVAATL	1840	1258	1.0483	10	14	100
VLTTSCGNTL	1841	2737	1.0505	10	11	79
VLVGGVLAAL	1842	1666	1.0492	10	12	86
VLVLNPSVAA	1843	1256		10	14	100
VMGSSYGFOY	1844	2639		10	11	79
VPESDAAARV	1845	1940	15.0241	10	12	86
VQWNNRLJAF	1846	1918		10	14	100
VGVVCAAIL	1847	1898		10	11	79
WVLVGGVLA	1848	1665	40.0135	10	12	86
YKGSGGPL	1849	1165	1.0479	10	12	86
YLLPRGPRLL	1850	35	1.0469	10	13	93
YLVTRHADVI	1851	1136		10	11	79
YGDLG3SVF	1852	276		10	12	86
ALVGVWCAAI	1853	1896		11	11	79
APTSGKSTKV	1854	1235	29.0117	11	13	93
APTLWARMILM	1855	2869	29.0118	11	11	79
AQAPPPSWDDM	1856	1602		11	12	86
AVCTRGVAKAV	1857	1188		11	11	79
AVQWNNRLJAF	1858	1917		11	14	100
DILAGYGAGVA	1859	1855		11	11	79
DLEWVTSWVL	1860	1657		11	12	86
DLGVRCERMA	1861	2617		11	13	93
DLMGVPLVGA	1862	132		11	11	79
DLVLTTRHADV	1863	1134		11	12	86
DOAETAGARLV	1864	1339		11	12	86
DKFFPGGGGV	1865	21		11	12	86
EDRKQKALGLL	1866	1731		11	12	86
FISGIOYLAGL	1867	1773		11	14	100
FLADGGGCSGA	1868	1304		11	11	79
FRGGGQGGV	1869	24		11	14	100
FGYSPGQRVEF	1870	2646	29.0119	11	14	100
GIQYLAGLSTL	1871	1776		11	11	79
GLPVQDHLFF	1872	1552		11	14	100
GLSTLPGNPAI	1873	1782		11	12	86
GPTLLYRLGA	1874	1625		11	11	79
GPWCFTPSPV	1875	507	29.0120	11	13	93
GVLAALAAAYCL	1876	1670	29.0121	11	12	86
GVRVCEKIALY	1877	2619		11	14	100

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
GVRLEDGNNY	1878	154		11	12	86
HLQNIIVQY	1879	696		11	11	79
HMMNFISQY	1880	1769		11	13	93
HQNIIVQYLY	1881	698		11	11	79
HVGFEGAVQW	1882	1910		11	11	79
ILGGWVAQLA	1883	1816		11	12	86
ILGIGTVLDOA	1884	1331		11	12	86
ILSPGALVGV	1885	1891		11	13	93
KPARLVFPDL	1886	2608	29.0122	11	11	79
KPTLHGPTLL	1887	1620	29.0123	11	11	79
KOKALGLQTA	1888	1734		11	12	86
KVIDTLTCGFA	1889	121		11	12	86
KVLVNFSAVA	1890	1255		11	14	100
LIAFASRGNHV	1891	1924		11	14	100
LITSCSNVSV	1892	2815		11	14	100
LVPFDLGVRV	1893	2612		11	11	79
LLFILLADRV	1894	726		11	13	93
LLFNILGGWVA	1895	1812		11	12	86
LLPAILSPGAL	1896	1887		11	13	93
LLPRGPRLGV	1897	36		11	13	93
LLSPRGSRPSW	1898	97		11	11	79
LLWRQEMGNI	1899	2240		11	12	86
LPAILSPGALV	1900	1888	29.0124	11	12	86
LPALSTGLJHL	1901	687	29.0125	11	12	86
LPQCSFSIFLL	1902	169	29.0126	11	13	93
LPVQDHLERW	1903	1553	29.0127	11	12	86
LVGGVLAALAA	1904	1667		11	12	86
LVLNPSVAATL	1905	1257		11	14	100
LVTRHADVPV	1906	1137		11	11	79
LVGWVCAAIL	1907	1897		11	11	79
NILGGWVAACL	1908	1815		11	12	86
NITRVSENVK	1909	2249		11	12	86
NLLPAILSPGA	1910	1886		11	13	93
NLPQCSFSIFL	1911	168		11	13	93
PITYSTYQKFL	1912	1295		11	11	79
PLEGERGDFDL	1913	2403		11	13	93
PMGFSYDTRCF	1914	2667		11	11	79
PFSWDQMKKCL	1915	1606	29.0128	11	11	79
PVNSWLGNIIM	1916	2857		11	12	86
PVYCFTRSPVV	1917	508		11	13	93
RMVGGVGRHL	1918	635		11	13	93
RQEMGGNTRV	1919	2243		11	12	86
RVCCKMALYDV	1920	2621		11	12	86
SIFLLALLSCL	1921	175		11	12	86
SMLTDPSHITA	1922	2178		11	14	100

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
SPTHVPESDA	1923	1935	29.0129	11	12	86
SQPCPEPDV	1924	2163		11	12	86
SVAATLGFAY	1925	1262		11	14	100
TLGFGAYMSKA	1926	1266		11	12	86
TLFRNLGGWV	1927	1811	29.0130	11	12	86
TFCTGSSDLY	1928	1126		11	11	79
TFGLPVQDHL	1929	1550		11	13	93
TPVNSWLGNI	1930	2856		11	12	86
TVLDOAETAGA	1931	1336	29.0132	11	12	86
VLCECYDAGCA	1932	1521		11	11	79
VLVDILAGYGA	1933	1852		11	11	79
VLVGGVLAALA	1934	1666		11	12	86
VQPEKGGKPA	1935	2600	1918	11	11	79
VQMMNRLIAFA	1936	1918		11	14	100
VVCAAILRRHV	1937	1901		11	11	79
WVLVGGVLAAL	1938	1665		11	12	86
YLGSSGGHLL	1939	1165	1590	11	12	86
YLVAYQATVCA	1940	1590		11	12	86
YQATVCARAQA	1941	1594		11	11	79
YVGLGGSVFL	1942	276		11	12	86
YVPESDAAARV	1943	1939		11	12	86

Table XV
HCV A01 Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101
ASFCGSPY	1944	166	26.0026	8	20	100	
DSNVLRSKY	1945	737	20.0255	10	18	90	0.0001
FAAPFTQCGY	1946	631	20.0254	10	19	95	0.0680
GFAAPFTQCGY	1947	630		11	19	95	
GRETVEY	1948	140		8	15	75	
GYSNFMGY	1949	579	2.0058	9	17	85	
HTLWKAGILY	1950	149	1069.04	10	20	100	0.1100
KQAFTRSPY	1951	653	20.0256	10	19	95	0.0001
LLDTASALY	1952	30	1069.01	9	17	85	12.0000
LSLDVSAAFY	1953	415	1090.07	10	19	95	0.0150
LTRGRETVEY	1954	137		11	15	75	
MMWYWGSPSY	1955	360	1039.01	10	17	85	0.0810
MSTIDLEAY	1956	103	2.0126	9	15	75	0.8500
NSWLSRKY	1957	738	2.0123	9	18	90	0.0005
PLDKGKPY	1958	124	1147.12	9	20	100	
PLDKGKPY	1959	124	1069.03	10	20	100	0.1700
PTTGRTSLY	1960	797	1090.09	9	17	85	0.2100
SASFCGSPY	1961	165		9	20	100	
SLDVSAAFY	1962	416	1069.02	9	19	95	5.2000
STTDLEAY	1963	104		8	15	75	
TTGRTSLY	1964	798	26.0030	8	17	85	
WLSLDVSAAFY	1965	414	26.0551	11	19	95	
WMMWYWGFS	1966	359	1039.06	11	17	85	0.3200
YPALMPLY	1967	640	19.0014	8	19	95	
YSLNFMGY	1968	580	26.0032	8	17	85	

Table XVI
HCV A03 Motif with Binding Information

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12	24.0103	.	647	10	AACNWTGRGER	1969	0.0003
79	11			147	10	AARALAHGVR	1970	
100	14			1264	8	AATLGFGA	1971	
100	14			1264	9	AATLGFAY	1972	
79	11			1187	9	AAVCTRGVA	1973	
79	11			1187	10	AAVCTRGVAK	1974	
79	11			1187	11	AAVCTRGVAKA	1975	
86	12			648	9	ACNWTGRGER	1976	
79	11			1306	9	ADGGCSGA	1977	
79	11			1306	10	ADGGCSGAY	1978	
86	12			1142	8	ADVIPVRR	1979	
79	11			1142	9	ADVIPVRRR	1980	
100	14			1926	8	AFASRGNH	1981	
86	12			1865	8	AGALVAFK	1982	
86	12			1344	9	AGARLVVLA	1983	
79	11			1344	11	AGARLVVLATA	1984	
100	14			1781	11	AGLSTLPGNPA	1985	
86	12			1862	9	AGVAGALVA	1986	
86	12			1862	10	AGVAGALVAF	1987	
86	12			1862	11	AGVAGALVAFK	1988	
86	12			94	8	AGWLLSPR	1989	
86	12			94	11	AGWLLSPRGR	1990	
86	12			1858	8	AGYGAGVA	1991	
86	12			1858	10	AGYGAGVAGA	1992	
86	12			1737	8	ALGLLOTA	1993	
86	12			689	8	ALSTGLIH	1994	
86	12			689	10	ALSTGLIHLH	1995	0.0003
79	11	24.0104		1896	9	ALVGVWCA	1996	
79	11	40.0089		1896	10	ALVGVWCAA	1997	
79	11			1793	8	ASLMAFTA	1998	
79	11			2208	10	ASQLSAPSLK	1999	
79	11			2208	11	ASQLSAPSLKA	2000	
86	12			1928	11	ASRGNHVSPTH	2001	
100	14			2204	10	ASSSASQLSA	2002	
93	13			165	10	ATGNLPGCSF	2003	
100	14			1265	8	ATLGFAY	2004	
86	12			1265	11	ATLGFAYMSK	2005	
79	11			48	8	ATRKTSER	2006	
79	11			1596	9	ATVCARAQA	2007	
79	11			1188	8	AVCTRGVA	2008	
79	11	1090.23		1188	9	AVCTRGVAK	2009	0.0260
79	11			1188	10	AVCTRGVAKA	2010	
100	14			1917	10	AVQWMNRLIA	2011	
100	14			1917	11	AVQWMNRLIAF	2012	
93	13			1903	8	CAAILRRH	2013	

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			1530	9	CAWYELTPA	2014	
93	13			128	9	CGFADLMGY	2015	
79	11			2742	8	CGNTLTCY	2016	
79	11			1130	11	CGSSDLYLVR	2017	
100	14			2727	8	CGYRRCRA	2018	
86	12			2941	11	CLRKLGVPPLR	2019	
100	14			172	9	CSFSIFLLA	2020	
100	14			2819	8	CSSNVSA	2021	
86	12			2819	9	CSSNVSAH	2022	0.0001
79	11	1069.62		1128	9	CTCGSSDLY	2023	
79	11			1190	8	CTRGVAKA	2024	
79	11			1190	11	CTRGVAKAVDF	2025	
79	11			555	9	CTWVNSTGTF	2026	
79	11	3.0438		555	11	CTWVNSTGFTK	2027	0.7600
79	11	1.0961		2599	9	CVQPEKGR	2028	0.0008
79	11	1.0501		2599	10	CVQPEKGRK	2029	0.0011
86	12			1462	8	CVTQTVDF	2030	
100	14	24.0076		1574	9	DAFLSQTK	2031	0.0003
79	11			2771	10	DDLWICESA	2032	
100	14			1468	8	DFSLDPTF	2033	
79	11			1307	8	DGGCGGA	2034	
79	11			1307	9	DGGCGGGAY	2035	
86	12			1316	9	DIICDECH	2036	
86	12			1855	8	DILAGYGA	2037	
79	11			1855	11	DILAGYGAGVA	2038	
93	13	1.0144		2617	9	DLGVRVCEK	2039	0.0003
93	13			2617	11	DLGVRVCEKMA	2040	
79	11			132	11	DLMGYPILVGA	2041	
79	11			1883	8	DLVNLPLA	2042	
79	11			2772	9	DLWICESA	2043	
79	11			1134	8	DLYLVTRH	2044	
86	12			1134	9	DLYLVTRHA	2045	0.0003
86	12	24.0074		124	8	DTLTCGFA	2046	
79	11			1143	8	DVIPVRRR	2047	
100	14			2794	8	EAMTRYSA	2048	
79	11			1524	8	ECYDAGCA	2049	
79	11			1524	10	ECYDAGCAWY	2050	
79	11			1882	9	EDLVNLLPA	2051	
100	14	24.0077		1915	9	EGAVQWMMR	2052	0.0004
93	13			1377	8	EIPFYGKA	2053	
86	12			2245	8	BMGGNTR	2054	
86	12			1342	11	ETAGARLVLA	2055	
86	12			1207	9	ETTMFSPVF	2056	
86	12	1090.24		2596	9	EVFCVQPEK	2057	0.0008
79	11			2598	10	FOVQPEKGR	2058	

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			2598	11	FCVQPEKGGFK	2059	
86	12			1269	8	FGAYMSKA	2060	
86	12			1269	9	FGAYMSKAH	2061	
79	11			553	11	FGCTWMNSTGF	2062	
86	12	1.0960		2554	9	FGYGAKVIR	2063	0.0008
100	14	40.0082		1773	9	FISGIQYLA	2064	
79	11			1304	11	FLADGGCSGGA	2065	
100	14			728	8	FLLADAR	2066	
79	11			2670	8	FSYDTRCF	2067	
100	14			2792	8	FTEAMTRY	2068	
100	14			2792	10	FTEAMTRYSA	2069	
93	13			1567	9	FTGLTHIDA	2070	
93	13			1567	10	FTGLTHIDAH	2071	
93	13			1567	11	FTGLTHIDAHF	2072	
79	11			146	8	GAARALAH	2073	
79	11			146	11	GAARALAHGVR	2074	
86	12			1861	10	GAGVAGALVA	2075	
86	12			1861	11	GAGVAGALVAF	2076	
86	12			350	8	GAHWGVLA	2077	
79	11			1895	10	GALVVGWCA	2078	
79	11			1895	11	GALVVGWCAA	2079	
86	12			1345	8	GARLVLA	2080	
79	11			1345	10	GARLVLATA	2081	
100	14			1916	8	GAVQWMNR	2082	
100	14			1916	11	GAVQWMNRLIA	2083	
86	12			1270	8	GAYMSKAH	2084	
79	11			1529	10	GCANYELTPA	2085	
100	14			171	10	GCSFIFLLA	2086	
79	11			554	10	GCTWMNSTGF	2087	
79	11			2770	11	GDLLWICESA	2088	
86	12			278	8	GDLOGSVF	2089	
93	13			129	8	GFADLMGY	2090	
86	12			1268	8	GFGAYMSK	2091	
86	12			1268	9	GFGAYMSKA	2092	
86	12			1268	10	GFGAYMSKAH	2093	
79	11			2645	9	GFCYSPGQR	2094	
79	11			2669	9	GFSYDTRCF	2095	
79	11			145	8	GGAARALA	2096	
79	11			145	9	GGAARALAH	2097	
79	11			1308	8	GGCSGGAY	2098	
100	14			26	10	GGQVGGVY	2099	
79	11			935	8	GGHYVOMA	2100	
100	14			27	9	GGQVGGVY	2101	
100	14	24.0078		1392	9	GGRIHJFCH	2102	0.0003
100	14			1392	11	GGRIHJFCHSK	2103	

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			2605	11	GGKPKARLIVF	2104	
86	12			1669	8	GGVLAALA	2105	
86	12			1669	9	GGVLAALAA	2106	
86	12			1669	10	GGVLAALAA	2107	
93	13			32	8	GGVLLPR	2108	
93	13	24.0080		32	9	GGVLLPRR	2109	0.0003
86	12			1818	9	GGWVAQLA	2110	
100	14			1333	9	GIGTVLDOA	2111	
79	11			3037	8	GNYLLPNR	2112	
93	13			1552	8	GLPVQDQH	2113	
86	12			1552	11	GLPVQDQHLEF	2114	
79	11			1004	8	GLPVSARR	2115	
79	11			968	8	GLRDLAVA	2116	
79	11			2921	8	GLSAFSLH	2117	
79	11	1073.03		2921	10	GLSAFSLHSY	2118	0.0100
100	14			1782	10	GLSTLPGNPA	2119	
93	13			1569	8	GLTHIDAH	2120	
93	13			1569	9	GLTHIDAHF	2121	
86	12			1238	10	GSGKSTKPPA	2122	
86	12			1238	11	GSGKSTKPPAA	2123	
86	12			1131	10	GSSDLVLTTR	2124	
86	12			1131	11	GSSDLVLTTRH	2125	
79	11			2641	8	GSSYGFQY	2126	
79	11			2063	8	GTFPINAY	2127	
100	14			1335	10	GTVLDOAETA	2128	
86	12			1863	8	GVAGALVA	2129	
86	12			1863	9	GVAGALVAF	2130	
86	12	1073.10	*	1863	10	GVAGALVAFK	2131	0.3900
79	11			1193	8	GVAKAVDF	2132	
79	11			1081	8	GVQWTVYH	2133	
79	11			1081	10	GVQWTVYHGA	2134	
79	11	1090.25	*	3035	10	GVGIYLPNR	2135	0.0014
86	12			1670	8	GVLAALAA	2136	
86	12	1174.19	*	1670	9	GVLAALAA	2137	0.0046
79	11			45	11	GVRATRTSER	2138	
100	14			2619	9	GVRVCEKMA	2139	
100	14			2619	11	GVRVCEKMALY	2140	
86	12			154	11	GVRVLEDGMY	2141	
79	11			1900	9	GWCAAILR	2142	
79	11			1900	10	GWCAAILRR	2143	
79	11			1900	11	GWCAAILRRH	2144	
93	13			33	8	GWYLLPRR	2145	
93	13			33	11	GWYLLPRRR	2146	
79	11			1141	8	HADVIPVR	2147	
79	11			1141	9	HADVIPVR	2148	

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			1141	10	HADVIPVRRR	2149	
100	14			1234	8	HAPTGSGK	2150	
93	13			1234	11	HAPTGSGKSTK	2151	
79	11			2920	9	HGLSAFSLH	2152	
79	11			2920	11	HGLSAFSLHSY	2153	
79	11			1624	8	HGPTPLLY	2154	
79	11			1624	9	HGPTPLLYR	2155	
100	14			1572	11	HIDAHFLSQTK	2156	
86	12	1073.16	*	1292	10	HLHAPTSGSK	2157	0.5900
79	11			696	11	HLHQNIVDQY	2158	
100	14			1395	8	HLIFCHSK	2159	
100	14	1090.26	*	1395	9	HLIFCHSKK	2160	0.0250
100	14	1073.12	*	1395	10	HLIFCHSKKK	2161	0.0260
93	13			1769	11	HMMNFSGIQY	2162	
100	14			1400	10	HSKKKODELA	2163	
100	14			1400	11	HSKKKODELAA	2164	
79	11			2928	10	HSYSPGEINR	2165	
79	11	1.1061		222	10	HTPGGVPCVR	2166	0.0004
79	11			1910	8	HVGPGEA	2167	
100	14	24.0079		1925	9	IAFASRGNH	2168	
100	14			1573	10	IDAHFLSQTK	2169	
86	12			123	8	IDTLTCGF	2170	
86	12			123	9	IDTLTCGFA	2171	
100	14			1397	8	IFCHSKKK	2172	
100	14			1334	8	IGTVLDQA	2173	
100	14			1334	11	IGTVLDQAETA	2174	
86	12			1317	8	IIDDECH	2175	
79	11	40.0140		1856	10	ILAGYGAGVA	2176	
86	12			1816	8	ILGGWVAA	2177	
86	12			1816	11	ILGGWVAAQLA	2178	
86	12			1331	11	ILGIGTVLDQA	2179	
86	12			2591	8	IMAKNEVF	2180	
100	14			1774	8	ISGIQYLA	2181	
86	12	1.0137	*	2250	9	ITRVESENK	2182	0.0150
100	14			2816	11	ITSCSSNVSVVA	2183	
86	12			989	8	ITWGADTA	2184	
86	12			989	9	ITWGADTAA	2185	
86	12			1296	8	ITYSTYK	2186	
86	12			1296	9	ITYSTYKGF	2187	
79	11			1296	11	ITYSTYKFLA	2188	
86	12			701	8	IVDVQYLY	2189	
86	12	1.0962		2613	9	IVFPDLGVR	2190	0.0036
93	13	1.1060		30	10	IVGGVYLLPR	2191	0.0008
93	13			30	11	IVGGVYLLPRR	2192	
86	12			1736	9	KALGLQTA	2193	

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12			1404	8	KDELAAK	2194	
86	12			2553	10	KFGYGAKDVR	2195	
79	11			1391	8	KGGRHLF	2196	
79	11			1391	10	KGGRHLFOH	2197	
79	11			2604	8	KGGRKPAR	2198	
79	11			2944	8	KLGVPLR	2199	
86	12			1241	8	KSTKVPAA	2200	0.0009
86	12	13.0016		1241	9	KSTKVPAAAY	2201	
86	12			1241	10	KSTKVPAAAYA	2202	
86	12			1241	11	KSTKVPAAAYAA	2203	
86	12			10	8	TKRNTNR	2204	
86	12	24.0085		10	9	TKRNTNRR	2205	0.0110
86	12	1.0952		51	9	KTSRSQPR	2206	0.1600
93	13			51	11	KTSRSQPRGR	2207	
86	12			121	10	KVIDTLTQGF	2208	
86	12			121	11	KVIDTLTQFA	2209	
86	12			1255	10	KVLVLPNSVA	2210	
100	14			1255	11	KVLVLPNSVAA	2211	
79	11			1244	8	KVPAAYAA	2212	
79	11			1305	10	LADGGCSGGA	2213	
79	11			1305	11	LADGGCSGGAY	2214	
86	12			1729	8	LAQRKQK	2215	
86	12			1729	9	LAQRKQKA	2216	
86	12			1857	9	LAGYGAGVA	2217	
79	11			1857	11	LAGYGAGVAGA	2218	
79	11			1522	10	LCECYDAGCA	2219	
79	11			1338	9	LDOAETAGA	2220	
86	12			1338	10	LDOAETAGAR	2221	
86	12			727	8	LFLLADA	2222	
100	14			727	9	LFLLADAR	2223	
100	14			1813	10	LFNLLGWVA	2224	
86	12			1813	11	LFNLLGGWVAA	2225	
79	11			290	8	LFTSPRR	2226	0.0810
86	12	24.0086		1267	9	LGFGAYMSK	2227	
86	12			1267	10	LGFGAYMSKA	2228	
86	12			1267	11	LGFGAYMSKAH	2229	
79	11			144	9	LGAARALA	2230	
79	11			144	10	LGAARALAH	2231	
79	11			1817	10	LGGWVAQA	2232	
86	12			1332	10	LGGWVAQAQA	2233	
93	13			44	8	LGGWVAQAQA	2234	
86	12			2618	8	LGVRAIRK	2235	
100	14			2618	10	LGVRAIRKMA	2236	
100	14			1924	10	LJAFASRGNH	2237	0.0008
100	14	1.0959		2235	9	LJAFASRGNH	2238	
86	12					LJAFASRGNH		

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
100	14			1396	8	LIFCHSKK	2239	
100	14	1.0123	.	1396	9	LIFCHSKK	2240	0.5400
79	11			414	9	LINTGSHH	2241	
79	11	1.1066		2612	10	LVPFOLGVR	2242	0.0003
100	14			1030	8	LLAPITAY	2243	
100	14	24.0071	.	726	9	LLFILLADA	2244	0.0016
100	14	1090.28	.	726	10	LLFILLADAR	2245	
100	14			1812	11	LLFNILGGWA	2246	
86	12			1887	10	LLFALLSPGA	2247	0.0003
93	13	24.0102		36	8	LLPRRGPR	2248	
93	13			97	8	LLSPRGSR	2249	
86	12			133	10	LMGYIPLVGA	2250	
79	11	13.0019	.	2922	9	LSAFSLHSY	2251	0.0002
79	11			2211	8	LSAPSLKA	2252	
79	11			2479	8	LSNSLLRH	2253	
86	12	24.0087		2479	9	LSNSLLRHH	2254	0.0003
86	12			690	9	LSTGLJLH	2255	
86	12			1783	9	LSTLPGNPA	2256	
100	14			126	11	LTCGFADLMGY	2257	
86	12			2180	9	LTDPSSHITA	2258	
100	14			1570	8	LTHDAHF	2259	
93	13			2176	10	LTSMLTDPH	2260	
93	13			1591	10	LVAYQATVCA	2261	
86	12	40.0133		1591	11	LVAYQATVCAR	2262	
79	11			1853	8	LVDILAGY	2263	
79	11	40.0139		1853	10	LVDILAGYGA	2264	
79	11			1667	8	LVGGVLAA	2265	
86	12			1667	10	LVGGVLAALA	2266	
86	12			1667	11	LVGGVLAALAA	2267	
86	12			1257	8	LVLNPSVA	2268	
100	14			1257	9	LVLNPSVAA	2269	
100	14			1897	8	LVGWVCA	2270	
79	11			1897	9	LVGWVCAA	2271	
79	11			2773	8	LWICESA	2272	
79	11			2668	8	MGFSYDTR	2273	
79	11			2668	10	MGFSYDTRCF	2274	
79	11			2640	9	MGSSYGQY	2275	
79	11			134	9	MGYIPLVGA	2276	
79	11			2876	8	MILMTHFF	2277	
86	12			2179	10	MLTDPSSHITA	2278	
100	14			1	9	MSTNPKQR	2279	
79	11			1	10	MSTNPKQRK	2280	
79	11			2726	8	NCGYRRCR	2281	
79	11			2726	9	NCGYRRCRA	2282	
79	11			305	8	NCSIVPGH	2283	

Conservancy	Freq.	Peptide	Filled	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
100	14			1772	8	NFSGIQY	2284	
100	14			1772	10	NFSGIQYLA	2285	
79	11			1080	8	NGVQWTVY	2286	
79	11			1080	9	NGVQWTVYH	2287	
79	11			1080	11	NGVQWTVYHGA	2288	
86	12			1815	8	NILGGWVA	2289	
86	12			1815	9	NILGGWVAA	2290	
86	12	1.0498		2249	10	NITRVESENK	2291	0.0010
86	12	1073.01		700	9	NIVDVQYLY	2292	0.0005
93	13			1886	11	NLLPAILSPGA	2293	
93	13			168	10	NLPGCSFSIF	2294	
86	12			1460	10	NTGVTQTVD	2295	
79	11			14	10	NTNRRPQDVK	2296	
79	11			14	11	NTNRRPQDKF	2297	0.0010
93	13			1549	11	NTPGLPVQDQH	2298	
93	13			1889	8	PAILSPGA	2299	
86	12			688	9	PALSTGLJH	2300	
86	12			688	11	PALSTGLJLH	2301	
79	11			1976	8	PCSGSWLR	2302	
79	11			1127	10	PCTGSSDLY	2303	
93	13			2616	10	PDLGNRVCEK	2304	
79	11			1894	11	PGALWGVVCA	2305	
100	14			170	8	PGCSFSIF	2306	
100	14			170	11	PGCSFSILLA	2307	
86	12			224	8	PGCVPCVR	2308	
93	13			1913	11	PGEGAVQMMNR	2309	
79	11			2932	8	PGEINRVA	2310	
86	12			1509	9	PGERFSGMF	2311	
100	14			25	11	PGGGQVGGWY	2312	
93	13			1551	9	PGLPVQDQH	2313	
100	14			79	8	PGYPWPLY	2314	
79	11			1295	9	PITYSTYK	2315	
79	11			1295	10	PITYSTYKGF	2316	
79	11			143	8	PLGGAARA	2317	
79	11			143	10	PLGGAARALA	2318	
79	11			143	11	PLGGAARALAH	2319	
93	13			1628	8	PLYRLGA	2320	
79	11			2667	9	PMGFSYDTR	2321	
79	11			2667	11	PMGFSYDTRCF	2322	
93	13			514	11	PSPVWGTDR	2323	
100	14			1261	9	PSVAATLGF	2324	
100	14			1261	11	PSVAATLGFGA	2325	
79	11			1607	8	PSWDQMWK	2326	
93	13			587	8	PTDCFRKH	2327	
86	12	1.0954		109	9	PTDPRRSR	2328	0.0008

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
93	13	1.0121		1236	9	PTGSGKSTK	2329	0.0002
86	12			1936	10	PTHYPESDA	2330	
86	12			1936	11	PTHYVPESDAA	2331	
79	11			1621	11	PTLHGPTLLY	2332	
93	13			1626	10	PTLLYRLGA	2333	
86	12			1554	9	PVQDHLEF	2334	
93	13	1.0956		516	9	PWVGTIDR	2335	0.0008
86	12			1340	8	QATAGAR	2336	
93	13			1595	8	QATVCARA	2337	
79	11			1595	10	QATVCARAQA	2338	
93	13			29	11	QWGGVLLPR	2339	
86	12			289	8	QLTFSPR	2340	
79	11	1.0955		289	9	QLTFSPRR	2341	0.7500
86	12			336	8	QLLRPOA	2342	
79	11			2210	8	QLSAPSLK	2343	
79	11			2210	9	QLSAPSLKA	2344	
86	12			1465	11	QTVDFSLDTF	2345	
79	11			1186	10	RAAVCTRGVA	2346	
79	11			1186	11	RAAVCTRGVAK	2347	
100	14			149	8	RALAHGVR	2348	
79	11			47	9	RATKTSER	2349	
86	12	24.0088		1930	9	RGNHWSPTH	2350	0.0003
86	12	24.0105		1930	10	RGNHWSPTHY	2351	0.0003
93	13			40	8	RGPRLGVR	2352	
93	13			40	9	RGPRLGVRA	2353	
79	11	24.0081		40	11	RGPRLGVRATR	2354	0.0120
93	13			59	9	RGRRQPIPK	2355	
86	12			1154	8	RGSLSPR	2356	
79	11			1192	9	RGVAKAVDF	2357	
79	11			43	8	RLGVRATR	2358	
79	11	1073.11		43	9	RLGVRATRK	2359	0.9400
86	12			2918	8	RLHLSAF	2360	
79	11			2918	11	RLHLSAFSLH	2361	
100	14			1923	8	RLIAFASR	2362	
100	14			1923	11	RLIAFASRGNH	2363	
79	11			2611	11	RLVFPDLGVR	2364	
86	12			1029	8	RLAPITA	2365	
86	12	1174.18		1029	9	RLAPITAY	2366	2.7000
86	12			1347	8	RLVVLATA	2367	
86	12			2875	8	RMILMTHF	2368	
86	12			2875	9	RMILMTHFF	2369	
100	14			635	9	RMVYGGVEH	2370	
100	14	1073.13		635	10	RMVYGGVEHR	2371	0.7200
93	13			55	8	RSQPRGR	2372	
100	14	1174.21		2621	9	RVCEKMALY	2373	0.1800

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12	1174.17	.	156	9	RVLEDGVNY	2374	0.0120
86	12			156	10	RVLEDGVNVA	2375	
79	11			2923	8	SAFSLSHY	2376	
79	11			2207	11	SASQLSAPSLK	2377	
100	14			2818	9	SCSSNVSA	2378	
86	12			2818	10	SCSSNVSAH	2379	
86	12			1133	8	SDLYLVTR	2380	
86	12			1133	9	SDLYLVTRH	2381	
86	12			1133	10	SDLYLVTRHA	2382	
100	14			173	8	SFSIFLA	2383	
86	12			1239	9	SGKSTKVPA	2384	
86	12			1239	10	SGKSTKVPAA	2385	
86	12			1239	11	SGKSTKVPAAY	2386	
100	14			2178	8	SMLTDPSSH	2387	
100	14			2178	11	SMLTDPSHITA	2388	
100	14			2206	8	SSASQLSA	2389	
86	12	24.0089		1132	9	SSDLYLVTR	2390	0.0003
86	12	24.0106		1132	10	SSDLYLVTRH	2391	0.0003
86	12			1132	11	SSDLYLVTRHA	2392	
86	12			2820	8	SSNVSAH	2393	
100	14			2205	9	SSASQLSA	2394	
86	12			691	8	STGUHLH	2395	
86	12			1242	8	STKVPAAY	2396	
86	12			1242	9	STKVPAAYA	2397	
79	11			1242	10	STKVPAAYAA	2398	
100	14			1784	8	STLPGNPA	2399	
79	11			2	8	STNPKPQR	2400	
79	11			2	9	STNPKPQRK	2401	
79	11			2	11	STNPKPQRKT	2402	
86	12			1663	11	STWLVGGVLA	2403	
86	12			1299	8	STYGKFLA	2404	
100	14			1262	8	SVAATLGF	2405	
100	14			1262	10	SVAATLGFGA	2406	
100	14			1262	11	SVAATLGFGAY	2407	
86	12			1343	10	TAGARLVVLA	2408	
93	13			127	10	TCGFADLMGY	2409	
79	11			1129	8	TCGSSDLY	2410	
79	11			1461	9	TCVTQTQDF	2411	
86	12			110	8	TDPRRSR	2412	
100	14			2181	8	TDPSHITA	2413	
79	11			1375	9	TGEIFFYK	2414	
79	11			1375	10	TGEIPFYGKA	2415	
93	13			1568	8	TGLTHIDA	2416	0.0003
93	13	24.0082		1568	9	TGLTHIDAH	2417	
93	13			1588	10	TGLTHIDAHF	2418	

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
93	13			166	9	TGNLPGCSF	2419	
93	13			1237	8	TGSGKSTK	2420	
86	12			1237	11	TGSGKSTK/PA	2421	
79	11			2590	9	TIMAKNEVF	2422	
86	12	1073.14	•	1266	10	TLGFGAYMSK	2423	0.0810
86	12			1266	11	TLGFGAYMSKA	2424	
79	11		•	1622	10	TLHGTPPLY	2425	0.0890
79	11	1073.04		1622	11	TLHGTPPLYR	2426	
79	11			686	11	TLPALSTGLIH	2427	
79	11			2871	11	TLWARMILMTH	2428	
100	14			2817	10	TSCSSNWSVA	2429	
86	12			2817	11	TSCSSNWSVAH	2430	
93	13			52	8	TSERSQPR	2431	
86	12	24.0107		52	10	TSERSQPRGR	2432	0.0003
86	12			52	11	TSERSQPRGRR	2433	
86	12			1050	8	TSLTGRDK	2434	
93	13	24.0083		2177	9	TSMITDP SH	2435	0.0003
79	11			2589	10	TTIMAKNEVF	2436	
86	12			1208	8	TVCARAGC	2437	
79	11			1597	8	TVDFSLDPTF	2438	
86	12			1466	10	TVLDOAETA	2439	
100	14			1336	9	TVLDOAETA	2440	
86	12			1336	11	TVLDOAETA	2441	
100	14			1263	9	VAATLGFGA	2442	
100	14			1263	10	VAATLGFGAY	2443	
86	12			1864	8	VAGALVAF	2444	
86	12	24.0090	•	1864	9	VAGALVAFK	2445	0.2400
86	12	40.0071		1592	9	VAYQATVCA	2446	
79	11	1.1064	•	1592	10	VAYQATVCAR	2447	0.0005
79	11			1592	11	VAYQATVCARA	2448	
79	11			1902	8	VCAAILRR	2449	
79	11			1902	9	VCAAILRRH	2450	
79	11			2622	8	VCEKMALY	2451	
100	14			505	8	VCGPVYCF	2452	
93	13			1555	8	VQDHLFF	2453	
86	12			1189	8	VCTRGVAK	2454	
79	11			1189	8	VCTRGVAKA	2455	
79	11			1082	9	VQWTVYHGA	2456	
100	14			1467	9	VDFSLDPTF	2457	
79	11			1854	9	VDILAGYGA	2458	
79	11			614	9	VDYPYRLWH	2459	
93	13			614	10	VDYPYRLWHY	2460	
86	12			2597	8	VFCVQPEK	2461	
79	11			2597	11	VFCVQPEKGR	2462	
79	11			2614	8	VFPOLGVR	2463	

Conservancy	Freq.	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
93	13			1566	10	VFTGLTHIDA	2484	
93	13			1566	11	VFTGLTHIDAH	2485	
86	12			277	9	VGLOGSVF	2486	
86	12			1668	10	VGGVLAALA	2467	
86	12			1668	10	VGGVLAALAA	2468	
86	12			1668	11	VGGVLAALAAY	2469	
93	13	24.0084		31	9	VGGVLLPR	2470	0.0003
93	13			31	10	VGGVLLPRR	2471	
79	11			3036	9	VGYLPNR	2472	0.0007
79	11	F104.01		1899	10	VGWCAAILR	2473	
79	11			1899	11	VGWCAAILRR	2474	
86	12			122	9	VIDTLTQGF	2475	
86	12			122	10	VIDTLTQGFA	2476	
86	12			1671	8	VLAALAAY	2477	
93	13			1521	8	VLCECYDA	2478	
79	11			1521	11	VLCECYDAGCA	2479	
100	14			1337	10	VLDQAETA	2480	
86	12			1337	11	VLDQAETAGA	2481	
86	12			1337	11	VLDQAETAGAR	2482	
86	12			157	8	VLEDGVNY	2483	
86	12			157	9	VLEDGVNYA	2484	
100	14			1258	8	VLNPSVAA	2485	
93	13			2175	11	VLTSMLTDPFH	2486	
79	11			1852	9	VLVDILAGY	2487	
79	11			1852	11	VLVDILAGYGA	2488	
86	12			1666	8	VLVGGVLA	2489	
86	12	24.0075		1666	9	VLVGGVLA	2490	0.0003
86	12			1666	11	VLVGGVLAALA	2491	
100	14			1256	9	VLVLPNSVA	2492	0.0003
100	14	24.0072		1256	10	VLVLPNSVAA	2493	
79	11			2639	8	VMGSSYGF	2494	
79	11			2639	10	VMGSSYGFQY	2495	
79	11			1138	11	VTRHADVPVR	2496	
79	11			1901	8	VVCAAILR	2497	
79	11			1901	9	VVCAAILRR	2498	
79	11			1901	10	VVCAAILRRH	2499	
79	11			1898	8	VWGWCA	2500	
79	11			1898	11	VWGWCAAILR	2501	
93	13			517	8	VWGTDDR	2502	
86	12			93	9	WAGWLLSPR	2503	
86	12			1766	8	WAKHMMWF	2504	
86	12			76	11	WAQFGYPMPLY	2505	
86	12			2873	9	WARMILMTH	2506	
86	12			2873	10	WARMILMTHF	2507	
86	12			2873	11	WARMILMTHFF	2508	

Table XVII

HCV All Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
AACNWRGER	2536	647	24.0103	10	12	86	0.0140
AARALAHGVR	2537	147		10	11	79	
AATLGFAY	2538	1264		9	14	100	
AAVCTRGVAK	2539	1187		10	11	79	
ACNWRGER	2540	648		9	12	86	
ADGGCGGAY	2541	1306		10	11	79	
ADVIPVR	2542	1142		8	12	86	
ADVIPVRR	2543	1142		9	11	79	
AFASRGNH	2544	1926		8	14	100	
AGALVAFK	2545	1865		8	12	86	
AGVAGALVAFK	2546	1862		11	12	86	
AGWLLSPR	2547	94		8	12	86	
AGWLLSPRGSR	2548	94		11	12	86	
ALSTGLIH	2549	689		8	12	86	
ALSTGLIHL	2550	689	24.0104	10	12	86	0.0027
ASQLSAPSLK	2551	2208		10	11	79	
ASRGNNVSPH	2552	1928		11	12	86	
ATLFGAY	2553	1265		8	14	100	
ATLFGAYMSK	2554	1265		11	12	86	
ATFKTSER	2555	48		8	11	79	
AVCTRGVAK	2556	1188	1090.23	9	11	79	0.0250
CAALRRH	2557	1903		8	13	93	
CGFADLMGY	2558	128		9	13	93	
CGNTLCY	2559	2742		8	11	79	
CGSSDLYLVR	2560	1130		11	11	79	
CLRLGVPLR	2561	2941		11	12	86	
CNCSYPGH	2562	304		9	11	79	
CNWRGER	2563	649		8	12	86	
CSSNVSAH	2564	2819		9	12	86	
CTCGSSDLY	2565	1128	1069.62	9	11	79	0.0063
CTWMNSTGFTK	2566	555	3.0438	11	11	79	0.7500
CYQPEKGGK	2567	2599	1.0961	9	11	79	0.0005
CYQPEKGGK	2568	2599	1.0501	10	11	79	0.0008
DAHFLSQTK	2569	1574	24.0076	9	14	100	0.0005
DGGCGGAY	2570	1307		9	11	79	
DIIDCECH	2571	1316		9	12	86	
DLGVRVCEK	2572	2617	1.0144	9	13	93	0.0002
DLYLVTRH	2573	1134		8	12	86	
DVIPVRR	2574	1143		8	11	79	
ECYDAGCANY	2575	1524		10	11	79	
EGAVQWNNR	2576	1915	24.0077	9	14	100	0.0014
EMGGNTR	2577	2245		8	12	86	
EVFOVQPEK	2578	2596	1090.24	9	12	86	0.0270
FOVQPEKGGK	2579	2598		10	11	79	
FOVQPEKGGK	2580	2598		11	11	79	

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
FGAYMSKAH	2581	1269		9	12	86	
FGYGADVR	2582	2554	1.0960	9	12	86	0.0005
ELLADAR	2583	728		8	14	100	
FTEAMTRY	2584	2792		8	14	100	
FTGLTHDAH	2585	1567		10	13	93	
GAARALAH	2586	146		8	11	79	
GAARALAHGVR	2587	146		11	11	79	
GAQMMNR	2588	1916		8	14	100	
GAYMSKAH	2589	1270		8	12	86	
GFADLMGY	2590	129		8	13	93	
GFGAYMSK	2591	1268		8	12	86	
GFGAYMSKAH	2592	1268		10	12	86	
GFOYSPGQR	2593	2645		9	11	79	
GGAARALAH	2594	145		9	11	79	
GGCSGGAY	2595	1308		8	11	79	
GGQMGGV	2596	26		10	14	100	
GGQMGGVY	2597	27		9	14	100	
GGRIHFCH	2598	1392	24.0078	9	14	100	0.0001
GGRIHFCHSK	2599	1392		11	14	100	
GGVLAALAAAY	2600	1669		10	12	86	
GGVLLPR	2601	32		8	13	93	
GGVLLPRR	2602	32	24.0080	9	13	93	0.0010
GYLLPNR	2603	3037		8	11	79	
GLPVQDQH	2604	1552		8	13	93	
GLPVSAFR	2605	1004		8	11	79	
GLSAFSLH	2606	2921		8	11	79	
GLSAFSLHSY	2607	2921	1073.03	10	11	79	0.0005
GLTHIDAH	2608	1569		8	13	93	
GNHVSPTH	2609	1931		8	12	86	
GNHVSPTHY	2610	1931		9	12	86	
GNITRVESENK	2611	2248		11	12	86	
GSSDLYLTR	2612	1131		10	12	86	
GSSDLYLTRH	2613	1131		11	12	86	
GSSYGFQY	2614	2641		8	11	79	
GTFPINAY	2615	2063		8	11	79	
GVAGALVAFK	2616	1863	1073.10	10	12	86	1.4000
GVCMTVYH	2617	1081		8	11	79	
GVGYLLPNR	2618	3035	1090.25	10	11	79	0.0140
GVLAALAAAY	2619	1670	1174.19	9	12	86	0.0110
GVRATRKTSER	2620	45		11	11	79	
GVRVCEKVALY	2621	2619		11	14	100	
GVRLEDGVNY	2622	154		11	12	86	
GVWCAAILR	2623	1900		9	11	79	
GVWCAAILRR	2624	1900		10	11	79	
GVWCAAILRRH	2625	1900		11	11	79	

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
GVIYLPVR	2626	33		8	13	93	
GWLPVRGPR	2627	33		11	13	93	
HADVIPVR	2628	1141		8	11	79	
HADVIPVR	2629	1141		9	11	79	
HADVIPVR	2630	1141		10	11	79	
HADVIPVR	2631	1234		8	14	100	
HADVIPVR	2632	1234		11	13	93	
HADVIPVR	2633	2920		9	11	79	
HADVIPVR	2634	2920		11	11	79	
HADVIPVR	2635	1624		8	11	79	
HADVIPVR	2636	1624		9	11	79	
HADVIPVR	2637	1572		11	14	100	
HADVIPVR	2638	1232	1073.16	10	12	86	0.0024
HADVIPVR	2639	696		11	11	79	
HADVIPVR	2640	1395		8	14	100	
HADVIPVR	2641	1395	1090.26	9	14	100	0.0006
HADVIPVR	2642	1395	1073.12	10	14	100	0.0002
HADVIPVR	2643	1769		11	13	93	
HADVIPVR	2644	2928		10	11	79	
HADVIPVR	2645	222	1.1061	10	11	79	0.0012
HADVIPVR	2646	1925	24.0079	9	14	100	0.0003
HADVIPVR	2647	1573		10	14	100	
HADVIPVR	2648	1397		8	14	100	
HADVIPVR	2649	1317		8	12	86	
HADVIPVR	2650	415		8	11	79	
HADVIPVR	2651	2250	1.0137	9	12	86	0.0079
HADVIPVR	2652	1296		8	12	86	
HADVIPVR	2653	701		8	12	86	
HADVIPVR	2654	2613	1.0962	9	11	79	0.0044
HADVIPVR	2655	30	1.1060	10	13	93	0.0056
HADVIPVR	2656	30		11	13	93	
HADVIPVR	2657	1404		8	12	86	
HADVIPVR	2658	2553		10	12	86	
HADVIPVR	2659	1391		10	11	79	
HADVIPVR	2660	2604		8	11	79	
HADVIPVR	2661	2944		8	12	86	
HADVIPVR	2662	2594		11	11	79	
HADVIPVR	2663	1241	13.0016	9	12	86	0.0001
HADVIPVR	2664	10		8	12	86	
HADVIPVR	2665	10	24.0085	9	12	86	0.0100
HADVIPVR	2666	51	1.0952	9	13	93	0.0640
HADVIPVR	2667	51		11	12	86	
HADVIPVR	2668	1305		11	11	79	
HADVIPVR	2669	1729		8	12	86	
HADVIPVR	2670	1338		10	12	86	

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
LFLLLADAR	2671	727		9	14	100	
LFTSPRR	2672	290		8	11	79	
LGFGAYMSK	2673	1267	24.0086	9	12	86	0.2900
LGFGAYNSKAH	2674	1267		11	12	86	
LGGAAALAH	2675	144		10	11	79	
LGVRATRK	2676	44		8	12	86	
LGVRVCEK	2677	2618		8	14	100	
LIAFASRGNH	2678	1924		10	14	100	
LIEANLLWR	2679	2235	1.0959	9	12	86	0.0005
LIFCHSKK	2680	1396		8	14	100	
LIFCHSKKK	2681	1396	1.0123	9	14	100	0.1900
LINTGNSWH	2682	414		9	11	79	
LIVFPDLGVR	2683	2612	1.1066	10	11	79	0.0001
LLAPITAY	2684	1030		8	14	100	
LFLLLADAR	2685	726	1090.28	10	14	100	
LLPRGPR	2686	36		8	13	93	
LLSPRGSR	2687	97		8	12	86	
LSAFSLHSY	2688	2922	13.0019	9	11	79	0.0002
LSNSLLRH	2689	2479		8	12	86	
LSNSLLRH	2690	2479	24.0087	9	12	86	0.0001
LSTGLIHLH	2691	690		9	12	86	
LTCGFADLMGY	2692	126		11	12	86	
LTSMLTDPFH	2693	2176		10	13	93	
LVAYOATVCAR	2694	1591		11	11	79	
LVDILAGY	2695	1853		8	11	79	
MGFSYDTR	2696	2668		8	11	79	
MGSSYGFQY	2697	2640		9	11	79	
MNRLIAFASR	2698	1921		10	14	100	
MNSTGFTK	2699	558		8	11	79	
MSTNPKPOR	2700	1		9	11	79	
MSTNPKPQHK	2701	1		10	11	79	
NOGYRRCR	2702	2726		8	11	79	
NCSYFGH	2703	305		8	11	79	
NFISGIQY	2704	1772		8	14	100	
NGVCWTVY	2705	1080		8	11	79	
NGVCWTVYH	2706	1080		9	11	79	
NITRVESENK	2707	2249	1.0498	10	12	86	0.0062
NIVDVQYLY	2708	700	1073.01	9	12	86	0.0140
NTNRPPDVK	2709	14	2.0168	10	11	79	0.0007
NTPGLPVQDQH	2710	1549		11	13	93	
PALSTGLIHLH	2711	688		11	12	86	
PALSTGLIHLH	2712	688		11	12	86	
PCGGSWLR	2713	1976		8	11	79	
PCTGSSDLY	2714	1127		10	11	79	
PDLGVRVCEK	2715	2616		10	13	93	

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
PGGICVR	2716	224		8	12	86	
PGGAVQWMN	2717	1913		11	13	93	
PGGGQGGVY	2718	25		11	14	100	
PGLPVQJQH	2719	1551		9	13	93	
PGYPWPLY	2720	79		8	14	100	
PITYSTYK	2721	1295		9	11	79	
PLGGAAPALAH	2722	143		11	11	79	
PMGFSYDTR	2723	2667		9	11	79	
PNRTGVR	2724	1281		8	13	93	
PSPVVGTTDR	2725	514		11	13	93	
PSWDQMMK	2726	1607		8	11	79	
PTDPRKH	2727	587		8	13	93	
PTDPRRSR	2728	109	1.0954	9	12	86	0.0005
PTSGKSTK	2729	1236	1.0121	9	13	93	0.0001
PTLHGPTLLY	2730	1621		11	11	79	
PVWGTDDR	2731	516	1.0956	9	13	93	0.0005
QAETAGAR	2732	1340		8	12	86	
QINGGWLLPR	2733	29		11	13	93	
QLFTSPR	2734	289		8	12	86	
QLFTSPRR	2735	289	1.0955	9	11	79	0.0330
QLSAPSLK	2736	2210		8	11	79	
QNVIVQY	2737	699		8	11	79	
QNVIVQVLY	2738	699		10	11	79	
RAAVCTRGVAK	2739	1186		11	11	79	
RALAHGVR	2740	149		8	14	100	
RATRKTSER	2741	47		9	11	79	
RGNHNSPT	2742	1930	24.0088	9	12	86	0.0001
RGNHNSPTNY	2743	1930	24.0105	10	12	86	0.0001
RGPRLGVR	2744	40		8	13	93	
RGPRLGVRATR	2745	40		11	11	79	
RGRFQPIK	2746	59	24.0081	9	13	93	0.0017
RGSLLSPR	2747	1154		8	12	86	
RLGVRATR	2748	43		8	11	79	
RLGVRATR	2749	43	1073.11	9	11	79	0.0290
RLHGLSAFSLH	2750	2918		11	11	79	
RLIAFASR	2751	1923		8	14	100	
RLIAFASRGNH	2752	1923		11	14	100	
RLIVFPDLGVR	2753	2611		11	11	79	
RLLAIPITAY	2754	1029	1174.18	9	12	86	0.0270
RMVVGVEH	2755	635		9	14	100	
RMVVGVEH	2756	635	1073.13	10	14	100	0.0200
RYTNRRPDVK	2757	13		11	11	79	
RSQPRGR	2758	55		8	13	93	
RVCEKMY	2759	2621	1174.21	9	14	100	0.5000
RVLEDGNY	2760	156	1174.17	9	12	86	0.0068

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
SAFSLHSY	2761	2923		8	11	79	
SASQLSAPSLK	2762	2207		11	11	79	
SCSSNVSVAH	2763	2818		10	12	86	
SDLYLVTR	2764	1133		8	12	86	
SDLYLVTRH	2765	1133		9	12	86	
SGKSTKVPAAAY	2766	1239		11	12	86	
SMILDPFH	2767	2178		8	14	100	
SNLSLRHH	2768	2480		8	12	86	
SSDLYLVTR	2769	1132	24.0089	9	12	86	0.0044
SSDLYLVTRH	2770	1132	24.0106	10	12	86	0.0013
SSNWSVAH	2771	2820		8	12	86	
STGLHLH	2772	691		8	12	86	
STKVPAAY	2773	1242		8	12	86	
STNPKPOR	2774	2		8	11	79	
STNPKPORK	2775	2		9	11	79	
STNPKPORKTK	2776	2		11	11	79	
SVAATLGFAY	2777	1262		11	14	100	
TOGFADLMGY	2778	127		10	13	93	
TOGSSDLY	2779	1129		8	11	79	
TDPRRSR	2780	110		8	12	86	
TGEFFYFK	2781	1375		9	11	79	
TGLTHIDAH	2782	1568	24.0082	9	13	93	0.0001
TGSGKSTK	2783	1237		8	13	93	
TLGFAYMSK	2784	1266	1073.14	10	12	86	0.0610
TLHGPTPLLY	2785	1622	1073.04	10	11	79	0.0007
TLHGPTPLLYR	2786	1622		11	11	79	
TLPALSTGLIH	2787	686		11	11	79	
TLWARMILMTH	2788	2871		11	11	79	
TNPKPORK	2789	3		8	11	79	
TNPKPORKTK	2790	3		10	11	79	
TNPKPORKTKR	2791	3		11	11	79	
TNRRPDVK	2792	15		9	11	79	
TSCSSNVSVAH	2793	2817		11	12	86	
TSERSOPR	2794	52		8	13	93	
TSERSOPRGR	2795	52	24.0107	10	12	86	0.0001
TSERSOPRGRR	2796	52		11	12	86	
TSLTGDRK	2797	1050		8	12	86	
TSMILDPFH	2798	2177	24.0083	9	13	93	0.0001
VAATLGFAY	2799	1263		10	14	100	
VAGALVAFK	2800	1864	24.0090	9	12	86	0.8900
VAYOATVCAR	2801	1592	1.1064	10	11	79	0.0038
VCAAILRR	2802	1902		8	11	79	
VCAAILRRH	2803	1902		9	11	79	
VCEKMALY	2804	2622		8	14	100	
VCTRGVAK	2805	1189		8	11	79	

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
VDYPRLMH	2806	614		9	13	93	
VDYPRLWHY	2807	614		10	13	93	
VFCVPEK	2808	2597		8	12	86	
VFCVPEKGR	2809	2597		11	11	79	
VFPDLGV	2810	2614		8	11	79	
VFTGLTHDAH	2811	1566		11	13	93	
VGGVLAALAA	2812	1668		11	12	86	
VGGVLLPR	2813	31	24.0084	9	13	93	0.0019
VGGVLLPRR	2814	31		10	13	93	
VGYLPNR	2815	3036		9	11	79	
VGVCAAILR	2816	1899	F104.01	10	11	79	0.0100
VGVCAAILR	2817	1899		11	11	79	
VLAALAY	2818	1671		8	12	86	
VLDQAETAGAR	2819	1337		11	12	86	
VLEDGNY	2820	157		8	12	86	
VLTSMLTDPH	2821	2175		11	13	93	
VLVDILAGY	2822	1852		9	11	79	
VMGSSYGQY	2823	2639		10	11	79	
VTRHADVPVR	2824	1138		11	11	79	
VVCAAILR	2825	1901		8	11	79	
VVCAAILR	2826	1901		9	11	79	
VVCAAILRRH	2827	1901		10	11	79	
VVGWCAAILR	2828	1898		11	11	79	
VVGITDR	2829	517		8	13	93	
WAGWLLSPR	2830	93		9	12	86	
WAGQYWPFL	2831	76		11	12	86	
WARMILMTH	2832	2873		9	12	86	
WGPTDPRR	2833	107		8	12	86	
WGPTDPRR	2834	107		9	12	86	
WGPTDPRR	2835	107		11	12	86	
WLSPRGSR	2836	96	1.0953	9	12	86	0.0005
WNNRLAFASR	2837	1920		11	14	100	
WNNSTGFTK	2838	557	1174.16	9	11	79	0.0810
WNFSQY	2839	1771		9	14	100	
YDAGCAWY	2840	1526		8	11	79	
YDIICDECH	2841	1315		10	12	86	
YGFQYSPGQR	2842	2644		10	11	79	
YLLPRGPR	2843	35	1.0951	9	13	93	0.0005
YSPGENR	2844	2930		8	11	79	
YGGVGEHR	2845	637		8	14	100	
YWPESDAAR	2846	1939	1.1065	10	12	86	0.0001

Table XVIII

HCV A24 Motif with Binding InformationTable XVIII HCV A24 Motif with Binding Information

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*2401	Motif
86	12			319	AWDMMNW	2847		A24i
79	11	13.0132		1248	AYAAQGYKVL	2848	0.0009	A24i
100	14			1421	AYRGLDVSNI	2849		A24i
79	11			1525	CYDAGCAW	2850		A24i
79	11			1525	CYDAGCAWYEL	2851		A24i
100	14			1488	DFSLDPTF	2852		A24i
100	14			1488	DFSLDPTFTI	2853		A24i
86	12	24.0092	1996	1765	FWAKHWNF	2854	6.9000	A24i
86	12			1765	FWAKHWNFI	2855		A24i
93	13			129	GFADLMGYI	2856		A24i
79	11			129	GFADLMGYIPL	2857		A24i
79	11			2669	GFSYDTRCF	2858		A24i
79	11			1027	GWRLAPI	2859		A24i
86	12	13.0133		1859	GYGAGVAGAL	2860	0.0003	A24i
79	11	13.0131		135	GYPLVGAPL	2861	0.0057	A24i
86	12			2728	GYRRCRASGVL	2862		A24i
93	13	1174.08	1996	1769	HMWNFSIGI	2863		A24i
86	12			176	IFLLALLSCL	2864		A24i
86	12			2591	IMAKNEVF	2865		A24i
93	13			23	KFPGGGQI	2866		A24i
86	12			1813	LFNLGGW	2867		A24i
86	12			2872	LWARMILMTHF	2868		A24i
86	12			2241	LWRCEMGGNI	2869		A24i
86	12			1135	LYLVRHADI	2870		A24i
79	11			1770	MWNFSIGI	2871		A24i
100	14			1770	MWNFSIGIYL	2872		A24i
100	14	1073.18	1993	636	MYVGGVEHRL	2873	0.0270	A24i
100	14	24.0091	1996	1772	NFSIGIYL	2874	0.0170	A24i
79	11			2667	PMGFSYDTRCF	2875		A24i
86	12			1732	QFKQKALGL	2876		A24i
86	12			1732	QFKQKALGLL	2877		A24i
100	14			1919	QWNRLIAF	2878		A24i
100	14	13.0075	1995	1778	QYLAGLSTL	2879	0.0480	A24i
79	11	13.0134	1995	2647	QYSPQRIEF	2880	0.0180	A24i
79	11			2647	QYSPQRIEFL	2881		A24i
86	12			317	RMAWDMMNW	2882		A24i
86	12			2875	RMILMTHF	2883		A24i
86	12			2875	RMILMTHFF	2884		A24i
93	13			635	RMVGGVEHRL	2885		A24i
100	14			173	SFSIFLLAL	2886		A24i
100	14	24.0108		173	SFSIFLLALL	2887	0.0041	A24i
100	14	1174.10		2178	SMLTDPShi	2888		A24i
79	11			1608	SWDMWKKL	2889		A24i
86	12			1164	SYLKGSGGGL	2890		A24i
79	11			556	TWMINSTGF	2891		A24i

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*2401	Motif
86	12			1664	TWLVGGVL	2892		A24i
93	13			1297	TYSTYGKF	2893		A24i
86	12	13.0074	1995	1297	TYSTYGKFL	2894	0.0230	A24i
93	13			1566	VFTGLTHI	2895		A24i
79	11			2639	VMSSYGF	2896		A24i
93	13	1073.19	1993	34	VYLLPRGPRL	2897	0.0016	A24i
100	14			1920	WMNRLIAF	2898		A24i
100	14			1422	YYRGLDVSI	2899		A24i

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
FGAYMSKAH	3052	12	86	TLGFGAYMSKAHGVD	2900	1266		5	36
FGCTWMNST	3053	12	86	GNWFGCTWMNSTGFT	2901	550	1283.13	11	79
FKQKALGLL	3054	12	86	AEQFKQKALGLLQTA	2902	1730	1283.35	12	86
FLALISCL	3055	12	86	FSIFLLALLSCLTVP	2903	174		6	43
FPDLGVRVC	3056	11	79	LIVFPDLGVRVCEKM	2904	2612		11	79
FQVAHLHAP	3057	12	86	PQTFQVAHLHAPTGS	2905	1225	1283.19	6	43
FRAAVCTRG	3058	12	86	VQIFRAAVCTRGVAK	2906	1182		7	50
FSIFLLALL	3059	14	100	GCSFSIFLLALLSCL	2907	171	1283.09	12	86
FSLDPTFTI	3060	14	100	TVDFSLDPTFTIETT	2908	1466	1283.28	11	79
FTEAMTRYIS	3061	14	100	LKRVTEAMTRYISAPP	2909	2789		7	50
FTSPVVVG	3062	13	93	VYCFTPSPVVVGTTD	2910	509	1283.12	13	93
FTTLPALST	3063	11	79	PCSFTTLPALSTGLI	2911	681		9	64
FWAKHWMNF	3064	12	86	LEVFWAKHWMNFISS	2912	1762		3	21
IDAHLFSQT	3065	14	100	LTHIDAHFLSQTQQA	2913	1570		7	50
IDCNTCVTQ	3066	12	86	DSVIDCNTCVTQTVTD	2914	1454	1283.27	12	86
IDTLTCGFA	3067	12	86	GKVIDTLTCGFADLM	2915	120		12	86
JEANLLWRQ	3068	12	86	ADLJEANLLWRQEMG	2916	2233		7	50
IFLLALLSC	3069	14	100	SFSIFLLALLSCLTV	2917	173		6	43
ILGGWVAAQ	3070	12	86	LFNHLGGWVAAQLAP	2918	1813		8	57
ILGIGTVLD	3071	12	86	STILGIGTVLDQAE	2919	1328		8	57
ILRRHVGP	3072	11	79	CAAILRRHVGPGEA	2920	1903	1283.42	11	79
ILSPGALVV	3073	13	93	LPAILSPGALVVGTV	2921	1888		11	79
INAYTTGFC	3074	12	86	TFPINAYTTGFCIPS	2922	2064		8	57
IPLVGAPLG	3075	11	79	MGYIPLVGAPLGGAA	2923	134		10	71
ITRVESENK	3076	12	86	GGNITRVESENKVVI	2924	2247		10	71
ITSCSSNVS	3077	14	100	LELITSCSSNVVAH	2925	2813	1283.57	11	79
IVFPDLGVR	3078	11	79	ARLIVFPDLGVRVCE	2926	2610	1283.52	11	79
LAALAAAYCL	3079	12	86	GGVLAALAAAYCLTTG	2927	1669		8	57
LADGCGSGG	3080	11	79	GKFLADGCGSGGAYD	2928	1302		10	71
LAGLSTLPG	3081	14	100	IQYLAGLSTLPGNPA	2929	1777	1283.37	14	100
LAGYGAGVA	3082	11	79	VDILAGYGAGVAGAL	2930	1854		10	71
LATATPPGS	3083	12	86	LVVLATATPPGSVTV	2931	1348		9	64
LDPTFTIET	3084	12	86	DFSLDPTFTIETTIV	2932	1468		5	36
LDQAETAGA	3085	12	86	GTVLDQAETAGARLV	2933	1335	1283.23	12	86

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
LELITCSS	3086	13	93	EYDELEITCSSNV	2934	2810		13	93
LEVVTSTWV	3087	12	86	SADLEVVTSTWLVG	2935	1655		11	79
LFLLADAR	3088	14	100	VVLLFLLADARVCS	2936	724	1283.15	4	29
LGGWVAAQL	3089	12	86	FNILGGWVAAQLAPP	2937	1814		8	57
LGIGTVLDQ	3090	13	93	TTILGIGTVLDQAET	2938	1329		9	64
LGVRATRTK	3091	12	86	GPRLGVRATRTKTSER	2939	41		10	71
LGVRVCEKM	3092	14	100	FPDLGVRVCEKMALY	2940	2615	1283.53	11	79
LHGLSAFSL	3093	11	79	IERLHGLSAFSLHSY	2941	2916		6	43
LHGTPPLY	3094	11	79	KPTLHGTPPLYRLG	2942	1620	1283.32	11	79
LHQNVVDVQ	3095	12	86	LIHLHQNVVDVQVLY	2943	694		10	71
LHSYSPGEI	3096	11	79	AFSLHSYSPGEINRV	2944	2924	1283.60	11	79
LIAFASRGN	3097	14	100	MNRLIAFASRGNHVS	2945	1921	1283.44	12	86
LIEANLLWR	3098	12	86	DADLIEANLLWRQEM	2946	2232	1283.47	7	50
LIFCHSKK	3099	14	100	GRHLIFCHSKKCKDE	2947	1393	1283.25	14	100
LITSCSNV	3100	14	100	DLELITSCSNVSVA	2948	2812		13	93
LLALLSCLT	3101	12	86	SIFLLALLSCLTTPA	2949	175		5	36
LLFLLADA	3102	14	100	YVVLFLFLLADARVC	2950	723		5	36
LLFNILGGW	3103	12	86	QNTLLFNILGGWVAA	2951	1809		4	29
LLADARVC	3104	13	93	LLFLLADARVCACL	2952	726		9	64
LLPAILSPG	3105	13	93	LVNLLPAILSPGALV	2953	1884		10	71
LMGYPLVG	3106	11	79	FADLMGYPLVGAPL	2954	130		11	79
LNPSVAATL	3107	14	100	VLVLNPSVAATLFGF	2955	1256	1283.22	14	100
LPAILSPGA	3108	13	93	VNLLPAILSPGALVV	2956	1885		11	79
LPALSTGLI	3109	12	86	FTTLPALSTGLIHLH	2957	684	1283.14	11	79
LPRGRPLG	3110	13	93	VYLLPRGRPLGVRA	2958	34	1283.02	13	93
LRDLAVAVE	3111	11	79	HNGRLDLAVAVEPVV	2959	966		4	29
LRKLGVPPL	3112	12	86	ASCLRKLGVPPLRVW	2960	2939	1283.61	7	50
LSAFSLHSY	3113	11	79	LHGLSAFSLHSYSPG	2961	2919	1283.59	11	79
LSAPSLKAT	3114	11	79	ASQLSAPSLKATCTT	2962	2208	1283.46	7	50
LSNSLLRHH	3115	12	86	INALSNSLLRHHNMV	2963	2476		4	29
LSPGALVVG	3116	13	93	PAILSPGALVVGVC	2964	1889		11	79
LSPLLSTT	3117	11	79	RSELSPLLSTTTEWQ	2965	664		7	50
LSPRGRPS	3118	11	79	GWLLSPRGRPSWGP	2966	95		11	79
LSTGLIHLH	3119	12	86	LPALSTGLIHLHQNI	2967	687		10	71

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
LTCGFADLM	3120	12	86	IDLTCGFADLMGYI	2968	123	1283.05	12	86
LTHIDAHFL	3121	13	93	FTGLTHIDAHFLSQT	2969	1567	1283.30	13	93
LTSMLTDP	3122	13	93	VAVLTSMLTDPSSHIT	2970	2173		9	64
LVAYQATVC	3123	12	86	FFVLVAYQATVCARA	2971	1588		9	64
LVDILAGYG	3124	11	79	GKVLVDILAGYGAGV	2972	1850		9	64
LVGGVLAAL	3125	12	86	TWVLVGGVLAALAAAY	2973	1664	1283.34	12	86
LVLNPSVAA	3126	14	100	YKVLVLPNSVAAATLG	2974	1254		14	100
LVNLLPAIL	3127	11	79	TEDLVNLLPAILSPG	2975	1881		10	71
LVTRHADVI	3128	11	79	DLVLVTRHADVIPVR	2976	1134	1283.17	11	79
LVVGVVCAA	3129	11	79	PGALVVGVVCAAILR	2977	1894		11	79
LVVLATATP	3130	12	86	GARLVVLATATPPGS	2978	1345	1283.24	11	79
LWARMILMT	3131	12	86	APTLWARMILMTHTF	2979	2869		11	79
LWRQEMGNN	3132	12	86	ANLLWRQEMGNNITR	2980	2238	1283.48	12	86
LYRLGAVQN	3133	11	79	TPLLYRLGAVQNEVT	2981	1627		9	64
MAKNEVFCV	3134	12	86	TTIMAKNEVFCVQPE	2982	2589	1283.51	9	64
MAWDMMNW	3135	12	86	GHRMAWDMMNWSPPT	2983	315	1283.10	12	86
MGGNITRVE	3136	12	86	RQEMGGNITRVESEN	2984	2243	1283.49	12	86
MGYIPLVGA	3137	11	79	ADLMGYIPLVGAPLG	2985	131	1283.06	11	79
MLTDPSSHIT	3138	14	100	LTSMLTDPSSHITAET	2986	2176	1283.45	8	57
MNRLIAFAS	3139	14	100	VQWMNRLIAFASRGN	2987	1918		14	100
MTRYSPPG	3140	14	100	TEAMTRYSPPGDPP	2988	2793		10	71
MWNFISGIQ	3141	14	100	AKHMWNFISGIQYLA	2989	1767	1283.36	12	86
MYVGVGEHR	3142	14	100	KVRMYVGVGEHRLNA	2990	633		5	36
VAGALVAFK	3143	12	86	GAGVAGALVAFKVMS	2991	1861		7	50
VAHLHAPTG	3144	12	86	TFQVAHLHAPTGSOK	2992	1227		6	43
VATDALMTG	3145	12	86	VVVVATDALMTGYTG	2993	1437	35.0106	6	43
VAYQATVCA	3146	12	86	PYLVAAYQATVCARAQ	2994	1589		11	79
VCAAILRRH	3147	11	79	VGVVCAAILRRHVGP	2995	1899		10	71
VCEKMALYD	3148	14	100	GVRVCEKMALYDVVS	2996	2619	1283.54	11	79
VQDHLFEW	3149	12	86	GLPVCQDHLFEWESV	2997	1552	35.0109	6	43
VCTRGVAKA	3150	11	79	RAAVCTRGVAKAVDF	2998	1186	1283.18	11	79
VFCVQPEKG	3151	12	86	KNEVFCVQPEKGGRK	2999	2594		10	71
VFTDNSSPP	3152	11	79	RSFVFTDNSSPPAVP	3000	1211		10	71
VFTGLTHID	3153	13	93	WESVFTGLTHIDAHF	3001	1563	1283.29	6	43

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
VGGVLAALA	3154	12	86	WVLVGGVLAALAAAYC	3002	1665		12	86
VGGVYLLPR	3155	13	93	QIVVGGVYLLPRGRP	3003	28		13	93
VGSQPCPEP	3156	12	86	QYLVGSQPCPEPD	3004	2158		6	43
VGVVCAAIL	3157	11	79	ALVVGVVCAAILRRH	3005	1896		11	79
VIDCNTCVT	3158	12	86	FDSVIDCNTCVTQTV	3006	1453		12	86
VIDTLTCGF	3159	12	86	LGVVIDTLTCGFADL	3007	119	1283.04	11	79
VLAALAAAYC	3160	12	86	VGGVLAALAAAYCLTT	3008	1668		8	57
VLATATPPG	3161	13	93	RLVVLATATPPGSVT	3009	1347		9	64
VLEDGVNYA	3162	12	86	GVRVLEDGVNYATGN	3010	154	1283.07	12	86
VLNPSVAAT	3163	14	100	KVLVLNPSVAATLGF	3011	1255		14	100
VLTSMLTDP	3164	13	93	DVAVLTSMLTDPHSI	3012	2172		9	64
VLTTSCGNT	3165	11	79	ASGVLTTSCTGNTLTC	3013	2734		10	71
VLVDILAGY	3166	11	79	LGVVLVDILAGYGAG	3014	1849		10	71
VLVGGVLA	3167	12	86	STWVLVGGVLAALAA	3015	1663		12	86
VLVLNPSVA	3168	14	100	GYKVLVLNPSVAATL	3016	1253	1283.21	14	100
VNLLPAILS	3169	12	86	EDLVNLLPAILSPGA	3017	1882	1283.39	11	79
VPESDAAAR	3170	12	86	THYVPESDAAARVTQ	3018	1937		7	50
VTSTWVLVG	3171	12	86	LEVVTSTWVLVGGVL	3019	1658	1283.33	12	86
VVATDALMT	3172	11	79	DVVVATDALMTGYT	3020	1436	1283.26	6	43
VVCAAILRR	3173	11	79	VVGVCAILRRHVG	3021	1898		10	71
VVGVCACAI	3174	11	79	GALVVGVCACAILRR	3022	1895	1283.41	11	79
VVLATATPP	3175	12	86	ARLVLATATPPGSV	3023	1346		9	64
VYCFITSPV	3176	13	93	CGFYCFITSPVVVG	3024	506	1283.11	13	93
WAGWLLSPR	3177	12	86	GCGWAGWLLSPRGR	3025	90		5	36
WARMILMTH	3178	12	86	PTLWARMILMTHFFS	3026	2870	1283.58	11	79
WGADTAACG	3179	12	86	IITWGADTAACGDII	3027	988		6	43
WGPTDPRRR	3180	12	86	RPSWGPTDPRRRSRN	3028	104		10	71
WMNRLJAF	3181	14	100	AVQWMNRLJAFASRG	3029	1917	1283.43	14	100
WRLAPITA	3182	11	79	SKGWRLAPITAYAQ	3030	1025	1283.16	4	29
WTGALITPC	3183	11	79	SYTWTGALITPCAAE	3031	2456	1283.50	9	64
WYELTPAET	3184	12	86	GCAWYELTPAETTVR	3032	1529		5	36
YATGNLPGC	3185	12	86	GVNYATGNLPGCSFS	3033	161	1283.08	11	79
YCFITSPVV	3186	13	93	GPVYCFITSPVVVGT	3034	507		13	93
YDAGCAWYE	3187	11	79	CECYDAGCAWYELTP	3035	1523		10	71

Table XIX B										HCV DR Super Motif With Binding Data							
Core	Sequence	Core SeqID	Exemplary SeqID	Exemplary SeqID Num	Peptide No.	DR1	DR2w2.1	DR3	DR4w4	DR4w5	DR5w11	DR5w12	DR6w19	DR6w2	DF7	DF9	DRw5
NP5VAATL	3107	VLVNPSVAATLGG	2955	1283.22	1.8000	0.0120	0.0004			0.0035	0.0140		0.3100	0.0012	1.5000	3.2000	
NPALSPGA	3108	VNLPLSPGALV	2956	1283.14	4.3000	0.0036	0.0016		0.0071		0.0130		0.0002		0.0400	0.0310	
PPALSTGLH	3109	FTPLPALSTGLHLH	2957	1283.02	0.0140	0.4000	0.0360		-0.0014		0.0120		0.0001		-0.0003	0.0032	
FTPLRGRFLGVR	3110	VTLPLRGRFLGVR	2958														
HNLRLDLAVAVFV	3111	HNLRLDLAVAVFV	2959														
ASQRLKLGWPPRLRW	3112	ASQRLKLGWPPRLRW	2960	1283.61	1.0000	0.5800	0.0520	0.0051	0.0080	0.4900	0.0310	1.9000	0.0014	0.0730	0.0290	0.0087	
RKLGWPPRL	3113	LHGLSAPLSHSYSPG	2961	1283.59	1.6000				0.0095						0.0070		
SAFSLHSY	3114	ASQLSAPLSKATCTT	2962	1283.46	0.0150				0.0056						0.0006		
ASQLSAPLSKATCTT	3115	INALSNLSLRHNMV	2963														
SNLSLRH	3116	PALSPGALVGVVC	2964														
SPGALVGV	3117	RSELSPLLSTTEWQ	2965														
SPGALVGV	3118	GMLLSFRGSPSGNP	2966														
STGLHLH	3119	LPALSTGLHLHQM	2967														
TOGFAQLM	3120	IDLTLTGFAQLMGYI	2968	1283.05	0.0017				0.0024						-0.0003		
LTHDAFL	3121	FTGLTHDAFLSOT	2969	1283.30	0.7600	0.6200	0.1300		0.0005	0.0030	0.0083		0.0002	0.0500	0.1400	0.0056	
TSMLTDP	3122	VAVLTSMLTDPSSHIT	2970														
LVAYQATVC	3123	FPTLVATQATVCARA	2971														
GVLDLAGYG	3124	GKVLVDLAGYGAGV	2972														
LVGVGLAAL	3125	TWVLVGGVLAALAA	2973	1283.34	0.7700	0.0011	-0.0003		0.0015		0.0008		0.0001		0.0570	0.0058	
LVVNPSVAA	3126	YKVLVNPVVAATLG	2974														
LVNLLPAIL	3127	TEDLVNLPLPALSPG	2975														
LVLRTHADVI	3128	DLYLVTRHADVPVR	2976	1283.17	0.0081	0.0220	0.0011		0.0016		0.0076		0.0005		0.0810	0.0620	
LVGVGVCAA	3129	PGALVGVVCAALIR	2977														
LVVLATATP	3130	GARVLVATATPFGS	2978	1283.24	0.0300	0.0009	0.0004		0.8800		0.0084		0.0004		0.0440	0.0067	
LVWRLMUT	3131	APTLVARHLMTFFF	2979														
LVWDFGNGN	3132	ANLVWRDGMGMNTR	2980	1283.48	0.7000				0.0018						0.0022		
LVFLRGAVCN	3133	TFPLVRLGAVQNEVT	2981														
LVMAKNVFCV	3134	TFMANVFCVDFE	2982	1283.51	0.0014				0.0036						0.0025	0.0230	
LVMAKNVGMNWSPT	3135	GFRMANVGMNWSPT	2983	1283.10	0.0280	0.0015	0.0044		0.1600		0.0079		0.0080		0.0017		
LVGNTRVE	3136	ROEGNTRGENSEN	2984	1283.49	0.0001				-0.0003						-0.0002		
LVMSYFLUGA	3137	ADLVGTFPLGAPLG	2985	1283.06	0.0006				0.0060						0.0018		
LVMLTDPSSHIT	3138	LTSMLTDPSSHITAT	2986	1283.45	0.0004				0.0740						-0.0003		
LVMLRLFAFAS	3139	VCMANRLFAFASRGN	2987														
LVMTFSAPG	3140	TEAMTFSAPGSDPP	2988														
LVNFRSGQ	3141	AGMANFRSGQYLA	2989	1283.36	1.5000	0.0150	0.0570		0.0040	0.0600	0.0076		0.0004	0.0160	0.2300	0.2700	
LVNMGVGBRHLNA	3142	KVRMANMGVGBRHLNA	2990														
LVAGALVAFK	3143	GAGVAGALVAFKAMS	2991														
LVAILHAPTGS	3144	TFQVALHAPTGSQK	2992														
LVATDALMTGS	3145	VVVATDALMTGTYGS	2993	35.0106	0.0048	0.0047	0.0014	1.1000			0.0006		0.0029	0.0029	0.0400		
LVAYQATVCARAQ	3146	PVLVAYQATVCARAQ	2994														
LVCAAILRRHNGP	2995	VGWVCAAILRRHNGP	2995														
LVCAAILRRH	3147	GVRVCAAILRRHNGP	2996	1283.54	0.0022				0.0012						-0.0002		
LVCAAILRRH	3148	GVRVCAAILRRHNGP	2996														
LVCAAILRRH	3149	GLPVCAAILRRHNGP	2997	35.0109	0.0063				0.0077						0.0024		
LVCAAILRRH	3150	RAVCTRVKAKANDF	2998	1283.18	0.0100												
LVCAAILRRH	3151	NEVFOVPEKGGK	2999														
LVCAAILRRH	3152	RSPVFDKSSPPAVP	3000														
LVCAAILRRH	3153	WESVFTGLTHDAFH	3001	1283.29	0.0310				0.0068						0.0005		
LVCAAILRRH	3154	WVLVGGVLAALAAVC	3002														
LVCAAILRRH	3155	GQVGGVTLRRFGP	3003														
LVCAAILRRH	3156	QYLVGGVTLRRFGP	3004														
LVCAAILRRH	3157	ALVVGWCAAILRRH	3005														
LVCAAILRRH	3158	FQVDDCNTQYQTY	3006														
LVCAAILRRH	3159	LQVDDTLTGFAQL	3007	1283.04	0.0015				0.0086						0.0079		
LVCAAILRRH	3160	VGVVLAALAAAYCLIT	3008														
LVCAAILRRH	3161	RLVLAATATPPGSVT	3009														

Table XXa HCV DR 3A Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
FLADGGCSG	3205	11	79	YKFLADGGCSGGAY	3224	1301	10	71
PSLDTFTI	3206	14	100	TVDFSLDPTFTIETT	3225	1466	11	79
LEGEQDPD	3207	14	100	MPLEGEQDPDLSD	3226	2401	11	79
LPCPEPDV	3208	12	86	GSQPCPEPDVAVL	3227	2162	9	64
MAVDMMNTW	3209	12	86	GHRMAVDMMMNWSPT	3228	315	12	86
MLTDPSHI	3210	14	100	LTSMLTDPSHITAET	3229	2176	8	57
MSADLEVVT	3211	11	79	MACMSADLEVVTSTW	3230	1651	6	43
VATDALMTG	3212	12	86	VVVVATDALMTGYTG	3231	1437	6	43
VQDHLFEW	3213	12	86	GLPVCQDHLFEWESV	3232	1552	6	43
VFPDLGVRV	3214	11	79	RLIVFPDLGVRVCEK	3233	2611	11	79
VFTDNSSPP	3215	11	79	RSPVFTDNSSPPAVP	3234	1211	10	71
VLCECYDAG	3216	13	93	DSSVLCECYDAGCAW	3235	1518	10	71
VLVDILAGY	3217	12	86	GVRVLVDILAGYATGN	3236	154	12	86
VLEDGVNTA	3218	11	79	LGRVLVDILAGYAG	3237	1849	10	71
VQPEKGGRK	3219	11	79	VFCVQPEKGGRKPAR	3238	2597	11	79
YDLELITSC	3220	13	93	QPEYDLELITSCSN	3239	2808	11	79
YSIEPLDLP	3221	11	79	GACYYSIEPLDLPQII	3240	2902	6	43
YVGLCGSV	3222	12	86	SAMYVGLCGSVFLV	3241	273	8	57
YVPESDAAA	3223	12	86	PTHYVPESDAAARVT	3242	1936	12	86

HCV DR 3A Motif With Binding Information

Table XXb

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR3	DR1	DR2w2B1	DR2w2B2	DR4w4	DR4w15	DR5w11	DR6w19	DR7	DR8w2	DR9	DRw53
FLADGCS	3205	YQKFLADGCSGGAY	3224												
FSLDPTTI	3206	TVDSLSLDTFTIETI	3225		0.0001			0.1600				0.0005			
LEGEFGPD	3207	MPPLEGEFGDFLSD	3226	-0.0017											
LPCEPDV	3208	GSQLPCEPDVAVL	3227	-0.0017										0.0230	
MAWDMM	3209	GHMAWDMMNWSPT	3228		0.0280	0.0015	0.0044	0.1600	0.0079		0.0080	0.0017			
MLTDFSHIT	3210	LTSMLTDFSHITAEI	3229		0.0004			0.0740				-0.0003			
MSADLEV	3211	MACMSADLEVVTSTW	3230		0.0048	0.0047	0.0014		0.0006		0.0029	0.0400	0.0029		
VATDALMT	3212	VVVVATDALMTGYTG	3231	1.1000											
VQDHLF	3213	GLPVQDHLFWESV	3232	0.0063											
VFDLGV	3214	RLIVFDLGVRCVK	3233												
VFTDNSSPP	3215	RSPVFTDNSSPPAVP	3234												
VLCBCYA	3216	DSSVLCBCYDAGCAW	3235	-0.0017											
VLEDGVNY	3217	GVRVLEDGVNYATGN	3236		0.0007			0.0086				-0.0002			
VLVDILAGY	3218	LKKVLVDILAGYGAG	3237												
VQPEKGR	3219	VFCVQPEKGRKPAR	3238												
YDLELITSC	3220	QPEYDLELITSCSN	3239		0.0003			0.0004				-0.0002			
YSIEPLDLP	3221	GACYSIEPLDLPQII	3240												
YVGDLCGS	3222	SAMYYVGDLCGSVFLY	3241	-0.0017											
YVPESDAA	3223	PTHYVPESDAAARVT	3242	0.0220											

Table XXc HCV 3B Motif

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
FCSSKKKCD	3243	14	100	HLIFCHSKKKCDELA	3250	1395	14	100
FSYDTRCFD	3244	11	79	PMGFSYDTRCFDSTV	3251	2667	11	79
LAQPKQKA	3245	12	86	GMQLAEQPKQKALGL	3252	1726	8	57
LKPTLHGPT	3246	11	79	LIRLKPTLHGPTLL	3253	1616	10	71
VRATRKTS	3247	11	79	RLGVRAIRKTSERSQ	3254	43	10	71
YLVTRHADV	3248	12	86	SDLVLYVTRHADVIPV	3255	1133	11	79
MSTNPKFQR	3249		79					

Table XXII

HCV Analogs

AA	Sequence	SeqID Num	Fixed Nomen.	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	1° Anchor Fixer
9	RVXEKMALY	3642		N	N	Y	N	N	No
9	AVXTRGVAK	3643		N	N	Y	N	N	
9	EVFXIQPEK	3644		N	N	Y	N	N	
9	HLFXHKKK	3645		N	N	Y	N	N	
9	LPGXSFIF	3646		N	N	N	N	Y	
9	LIFXHSKKK	3647		N	N	Y	N	N	
10	VLAALAAAYXL	3648		N	Y	N	N	N	
10	HLFXHKKK	3649		N	N	Y	N	N	
10	AAXNWTGGER	3650		N	N	Y	N	N	1
10	YLLPRGPRV	3651	L2.LV10	N	Y	N	N	N	
9	FPGCSFSIF	3652		N	N	N	N	Y	
9	LPVCSFSIF	3653		N	N	N	N	Y	
9	LPVCSFSYF	3654		N	N	N	N	Y	
9	LPVCMFSIF	3655		N	N	N	N	Y	
9	LPVCSFSIF	3656		N	N	N	N	Y	
9	LPVCSFSF	3657		N	N	N	N	Y	
9	LPVCSFSII	3658		N	N	N	N	Y	
9	PPVHGGPI	3659		N	N	N	N	Y	
10	KPTLHGPTPI	3660		N	N	N	N	Y	
10	APTLWARMI	3661		N	N	N	N	Y	
9	SPRGSRPSI	3662		N	N	N	N	Y	
10	LPRIGPRLGI	3663		N	N	N	N	Y	
9	SPQORVERI	3664		N	N	N	N	Y	
9	LPVCSFSII	3665		N	N	N	N	Y	
9	DPRRSRFNI	3666		N	N	N	N	Y	
10	SPGALWGV	3667		N	N	N	N	Y	No
10	TPLLRLGAI	3668		N	N	N	N	Y	No
9	TISGVLWQV	3669		N	Y	N	N	N	No
9	SISGVLWQV	3670		N	Y	N	N	N	No
9	SLMAFTASV	3671		N	Y	N	N	N	No
9	GLPDCITMLV	3672		N	Y	N	N	N	No
10	KLVALGVNAV	3673		N	Y	N	N	N	No
10	YLLPSRGPKL	3674		N	Y	N	N	N	No
10	KLGLGLNAV	3675		N	Y	N	N	N	No
10	YVLPFRGPRL	3676	LV2.L10	N	Y	N	N	N	Rev
10	VFFNLLGGW	3677		N	Y	N	N	N	No
10	KLVSGLGVNAV	3678		N	Y	N	N	N	Rev
9	CINGVCWTA	3679	I2.VA9	N	Y	N	N	N	Rev
9	CANGVCWTV	3680	IA2.V9	N	Y	N	N	N	Rev

Table XXIII. Immunogenicity of identified supermotif-bearing peptides

Supermotif	Peptide	Seq ID	Sequence	Protein	Position	Immunogenicity				Transgenic mice ^b		
						Human ^a		Pape	overall	Frequency	Response	
						Barnaba; patients	Barnaba; contacts					
A2	1073.05	3256	LLFNILGGWV	NS4	1812	1/6	7/17	2/21	0/6	10/50	6/6	6.4 (1.7)
	1090.18	3257	FLLLADARV	NS1/E2	728	2/6	7/17	1/21	0/6	10/50	5/6	9.5 (3.0)
	1013.02	3258	YLVAYQATV	NS4	1590	1/6	4/17	1/21	0/6	6/50	5/6	8.5 (3.7)
	1090.22	3259	RLVPPDLGV	NS5	2578	2/6	5/17	0/21	0/6	7/50	0/6	-
	1013.1002	3260	DLMGYPLV	Core	132	2/6	7/17	1/21	1/6	11/50	5/6	8.8 (2.6)
	24.0073	3261	WMNRLIAFA	NS4	1920	1/6	3/17	2/21	1/6	7/50	0/6	-
	24.0075	3262	VLVGGVLA	NS4	1666	1/6	6/17	3/21	1/6	11/50	0/6	-
	1174.08	3263	HMWNFISGI	NS4	1769	3/6	3/17	2/21	0/6	8/50	6/6	6.4 (1.7)
	1073.06	3264	ILAGYGAGV	NS4	1851	2/6	3/17	0/21	0/6	5/50	3/6	54.7 (3.3)
	1073.07	3265	YLLPRRGPR	CORE	35	2/6	5/17	7/21	1/6	17/50	4/6	59.1 (7.2)
	24.0071	3266	LLFLLLLADA	NS1/E2	726	2/6	9/17	0/21	0/6	11/50	0/6	-
	1.0119	3267	YLVTRHADV	NS3	1131	6/6	10/17	0/21	1/6	17/50	0/6	-
	1.0952	3268	KTSESRQPR	CORE	51	2/16	1/4	3/12	0/6	6/38	3/6	23.4 (1.3)
	1073.11	3269	RLGVRATRK	CORE	43	4/16	1/4	7/12	1/6	13/38	3/6	42.2 (1.2)
	1.0955	3270	QLFTFSPPR	ENV	290	1/16	0/4	6/12	1/6	8/38		
	1073.13	3271	RMVYGGVEHR	NS1/E2	632	5/16	1/4	4/12	1/6	11/38	2/6	2.8 (1.1)
	1.0123	3272	LIFCHSKKK	NS3	1396	6/16	1/4	4/12	2/6	13/38	3/6	4.4 (1.1)
	1073.10	3273	GVAGALVAFK	NS4	1863	3/16	0/4	6/12	2/6	11/38	6/6	56.5 (1.7)
B7	24.0090	3274	VAGALVAFK	NS4	1864	4/16	1/4	6/12	0/4	11/38	1/6	7.1
	24.0086	3275	TLGFGAYMSK	NS3	1262	6/16		2/12	2/5	10/33		
	1145.12	3276	LPGCSFSIF	CORE	169			2	3/10	5		

Table XXIV. Human and murine MHC-peptide binding assays established using purified MHC molecules and gel filtration chromatography

Species		Antigen	Allele	Cell line	Radiolabeled peptide		Notes
					Source	Seq ID	
Human	A	A1	A*0101	Steinlin	Hu. J chain 102-110	3277	YTAVVPLVY
		A2	A*0201	JY	HBVc 18-27 F6->Y	3278	FLPSDYFPSV
		A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	3279	FLPSDYFPSV
		A2	A*0203	FUN	HBVc 18-27 F6->Y	3280	FLPSDYFPSV
		A2	A*0206	CLA	HBVc 18-27 F6->Y	3281	FLPSDYFPSV
		A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	3282	FLPSDYFPSV
		A3		GM3107	non-natural (A3CON1)	3283	KVFPYALINK
		A11		BVR	non-natural (A3CON1)	3284	KVFPYALINK
		A24	A*2402	KAS116	non-natural (A24CON1)	3285	AVIDNYNKF
		A31	A*3101	SPACH	non-natural (A3CON1)	3286	KVFPYALINK
		A33	A*3301	LWAGS	non-natural (A3CON1)	3287	KVFPYALINK
		A28/68	A*6801	C1R	HBVc 141-151 T7->Y	3288	STLPETYVVR
		A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	3289	FTQAGYPAL
		B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	3290	APRTLVL
		B8	B*0801	Steinlin	IIIVgp 586-593 Y1->F, Q5->R 60s	3291	FLKDYQLL
		B27	B*2705	LG2		3292	FRYNGLIHR
		B35	B*3501	C1R, BVR	non-natural (B35CON2)	3293	FPFKYAAAF
		B35	B*3502	TISI	non-natural (B35CON2)	3294	FPFKYAAAF
		B35	B*3503	EHM	non-natural (B35CON2)	3295	FPFKYAAAF
		B44	B*4403	PITOUT	EF-1 G6->Y	3296	AEMGKYSFY
		B51		KAS116	non-natural (B35CON2)	3297	FPFKYAAAF
		B53	B*5301	AMAI	non-natural (B35CON2)	3298	FPFKYAAAF
		B54	B*5401	KT3	non-natural (B35CON2)	3299	FPFKYAAAF
		Cw4	Cw*0401	C1R	non-natural (C4CON1)	3300	QYDDAVYKL
		Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	3301	YRHDGNNVL
		Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	3302	YRHDGNNVL
Mouse	D ^b	D ^b		EL4	Adenovirus E1A P7->Y	3303	SGPSNTYPEI
		K ^b		EL4	VSV NP 52-59	3304	RGYVFOGL
		D ^d		P815	HIV-IIIIB ENV G4->Y	3305	RGPYRAFTI
		K ^d		P815	non-natural (KdCON1)	3306	KFNPMKTYI
		L ^d		P815	HBVs 28-39	3307	IPQSLDSYWTSI

Table XXIV. Human and murine MHC-peptide binding assays established using purified MHC molecules and gel filtration chromatography

B. Class II binding assays		Radiolabeled peptide				Notes
Species	Antigen	Allele	Cell line	Source	Seq ID	Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	3308	YKYVVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	3309	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	3310	YAAFAAAKTAATAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	3311	YKTIAFDEEAR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	3312	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	3313	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	3314	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	3315	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	3316	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	3317	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	3318	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	3319	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	3320	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	3321	EALHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	3322	QYIKANAKFIGITE
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	3323	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	3324	PKYVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 1272-1284	3325	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	3326	YARFQSQTTLKQKT
	DQ3.1	DQA1*0301/DQB1*0301	PF	non-natural (ROIV)	3327	YAHAAHAAHAAHAAHAA
Mouse	IA ^b		DB27.4	non-natural (ROIV)	3328	YAHAAHAAHAAHAAHAA
	IA ^d		A20	non-natural (ROIV)	3329	YAHAAHAAHAAHAAHAA
	IA ^k		CH-12	HEL 46-61	3330	YNTDGSYDYGILQNSR
	IA ^s		LS102.9	non-natural (ROIV)	3331	YAHAAHAAHAAHAAHAA
	IA ^u		91.7	non-natural (ROIV)	3332	YAHAAHAAHAAHAAHAA
	IE ^d		A20	Lambda repressor 12-26	3333	YLEDARRKKAIYEKKK
	IE ^k		CH-12	Lambda repressor 12-26	3334	YLEDARRKKAIYEKKK

optimal assay pH is 4.5

no NEM in PI mix

optimal assay pH is 5.5

optimal assay pH is 5.0

optimal assay pH is 5.0

optimal assay pH is 5.0

Table XXVI: HCV-derived conserved high algorithm A*0201-binding peptides

Peptide	Molecule	1st Position	Seq ID	Sequence	Consv.	A2-supertype binding capacity (IC50 nM)					A2 XRN
						A*0201	A*0202	A*0203	A*0206	A*6802	
1073.05	NS4	1812	3335	LLFNILGGWV	85	4.2	113	3.2	19	33	5
1090.18	NS1/E2	728	3336	FLLADARV	92	18	90	149	247	111	5
1013.02	NS4	1590	3337	YLVAYQATV	85	20	39	16	82	33	5
1090.22	NS5	2611	3338	RLVFPDLGV	79	56	391	10	370	8000	4
1013.1002	CORE	132	3339	DLMGYPLV	79	80	4778	204	481	12	4
24.0073	NS4	1920	3340	WMNRLLAFA	100	122	130	3.3	1609	400	4
24.0075	NS4	1666	3341	VLVGGVLAA	85	185	331	32	308	3077	4
1174.08	NS4	1769	3342	HMWNFISGI	92	15	10750	77	132	7547	3
1073.06	NS4	1851	3343	ILAGYGAGV	79	116	143	5.0	755	889	3
1073.07	CORE	35	3344	YLLPRRGPRRL	92	125	6143	455	416	10256	3
24.0071	NS1/E2	726	3345	LLFLLLLADA	100	217	287	455	3364	3077	3
1.0119	LORF	1131	3346	YLVTRHADV	85	455	2048	3.6	71	3077	3
24.0065	NS4	1891	3347	ILSPGALVV	92	238	10750	27	1028	3077	2
1013.12	NS1/E2	686	3348	ALSTGLIHL	85	313	7167	45	18500	10256	2
939.14	NS1/E2	696	3349	HLHQNVVDV	85	500	3071	19	1370	10811	2
1090.21	NS5	2918	3350	RLHGLSAFSL	79	179	782	625	18500	12500	1

Table XXVII: HCV-derived conserved high algorithm A*03 and/or A*11 binding peptides

Peptide	Molecule	1st Position	Seq ID	Sequence	Consv.	A3-supertype binding capacity (IC50 nM)						
						A*03	A*11	A*3101	A*3301	A*6801	A3 XRN	A3 XRN
1.0952	CORE	51	3364	KTSESRQPR	92	69	94	67	1813	145	4	4
1073.11	CORE	43	3365	RLGVRATRK	79	12	207	429	-	-	3	3
1.0955	ENV1	290	3366	QLFTSPRR	79	15	182	621	3766	3	3	3
1073.13	NS1/E2	632	3367	RMVVGVEHR	100	15	300	95	9667	1778	3	3
1.0123	NS3	1396	3368	LIFCHSKK	100	20	32	2535	24167	333	3	3
1073.10	NS4	1863	3369	GVAGALVAFK	85	28	4	3273	26364	118	3	3
24.0090	NS4	1864	3370	VAGALVAFK	85	46	7	3750	11600	258	3	3
24.0086	NS3	1262	3371	LGFGAYMSK	85	136	21	2950	22308	222	3	3
1174.16	NS1/E2	557	3372	WMNSTGFTK	79	208	74	12857	690	1429	2	2
1073.14	NS3	1261	3373	TLGFGAYMSK	85	136	98	-	22308	8889	2	2
1090.23	LORF	1183	3374	AVCTRGVAK	79	423	240	16364	-	-	2	2
1090.24	NS5	2596	3375	EVFCVQPEK	85	13750	222	-	-	18	2	2
24.0103	NS1/E2	647	3376	AACNWTGRER	85	36667	429	400	5273	4444	2	2
1073.16	NS3	1232	3377	HLHAPTSGSK	85	19	2500	-	-	2857	1	1
1073.12	NS3	1395	3378	HLIFCHSKK	100	423	-	20000	-	-	1	1
1090.26	NS3	1395	3379	HLIFCHSKK	100	440	10000	-	-	8000	1	1

* A dash indicates IC50nM >30,000

Table XXVIII: HCV derived conserved B*0702 binding peptides

A. High conservancy 9- and 10-mer peptides.

Peptide	Molecule	1st Position	SEQ ID	Sequence	Consv.	B7-supertype binding capacity (IC50 nM)						
						B*0702	B*3501	B*51	B*5301	B*5401	B7 XRN	
1145.12	Core	169	3380	LPGCSFSIF	92	28	90	100	114	6667	4	
15.0048	E2	681	3381	LPALSTGLI	85	157	-	2.8	1500	20000	2	
15.0234	NS3	1620	3382	KPTLHGPTPL	79	3.9	-	27500	-	-	1	
15.0247	NS5	2835	3383	APTLWARMIL	79	6.3	-	5500	-	-	1	
15.0042	CORE	99	3384	SPRGSRPSW	79	14	-	11000	-	-	1	
15.0039	Core	57	3385	QPRGRRQPI	92	24	-	-	-	-	1	
15.0218	Core	37	3386	LPRRGPRLGV	92	29	-	6111	-	4000	1	
15.0060	NS5	2615	3387	SPGQRVEFL	79	46	-	27500	-	-	1	
15.0043	Core	111	3388	DPRRRSRNL	85	324	-	-	-	-	1	
15.0063	NS5	2835	3389	APTLWARMI	79	344	-	4583	-	-	1	
1292.17	NS5	2317	3390	PPVVHGCPL	79	393	-	-	-	-	1	
15.0239	NS4	1893	3391	SPGALVVGVV	79	423	-	3438	-	-	1	
15.0235	NS3	1621	3392	TPLLYRLGAV	92	458	-	6875	-	909	1	

Table XXVIII: HCV derived conserved B*0702 binding peptides

B. Additional HCV derived B7 supermotif peptides.

Peptide	Molecule	1st Position	SEQ ID	Sequence	Consv.	B7-supertype binding capacity (IC50 nM)				
						B*0702	B*3501	B*51	B*5301	B*5401 B7 XRN
29.0035	NS3	1378	3393	IPFYGKAI	92	458	-	46	-	50 3
29.0040	Core	37	3394	LPRRGPRRL	92	0.85	-	306	-	5000 2
29.0036	Core	137	3395	IPLVGAPL	79	13	2250	79	-	2857 2
16.0187	NS1/E2	680	3396	LPCSFTTLPA	64	423	24000	9167	-	15 2
29.0039	Core	169	3397	LPGCSFSI	92	500	200	932	620	6250 2
15.0219	Core	142	3398	APLGAARAL	71	9.5	-	-	-	12500 1
29.0031	NS5	2869	3399	APTLWARM	79	13	-	4583	-	4348 1
15.0231	NS3	1512	3400	RPSGMFDSSV	71	153	-	-	-	- 1
29.0085	NS5	2474	3401	LPINALNSL	57	220	18000	1170	-	11111 1
29.0037	NS5	2608	3402	KPARLIVF	85	367	-	3235	-	16667 1
15.0237	NS4	1789	3403	NPAIASLMAF	71	393	9000	5000	-	- 1
29.0118	NS5	2869	3404	APTLWARMILM	79	423	-	-	-	3030 1
29.0042	NS4	1720	3405	LPVIEQGM	85	423	-	1375	-	7692 1

C. Engineered analogs of B7 supermotif peptides.

Peptide	Molecule	1st Position	SEQ ID	Sequence	Consv.	B7-supertype binding capacity (IC50 nM)				
						B*0702	B*3501	B*51	B*5301	B*5401 B7 XRN
1145.12	Core	169	3406	LPGCSFSIF	92	28	90	100	114	6667 4
1292.24	Core	169	3407	LPGCSFSII		37	4364	5.3	262	1056 3
1145.13	Core	169	3408	FPGCSFSIF		19	1.6	132	3.2	6.7 5

* A dash indicates IC50 nM >30,000.

Table XXXII. Candidate HCV-derived HTL epitopes

Selection criteria	Peptide	SEQ ID	Sequence	Source	Conservancy	
					Total	Core
A. DR-supermotif conserved 15mers	1283.01	3641	GQIVGGVYLLPRRGPR	HCV Core 28	93	93
	1283.02	3466	VYLLPRRGPRLGVR	HCV Core 34	93	93
	1283.03	3467	GWLLSPRGSRPSWGPT	HCV Core 95	79	79
	1283.04	3468	LGKVIDTLTCGFADL	HCV Core 119	79	86
	1283.05	3469	IDTLTCGFADLMGYI	HCV Core 123	86	86
	1283.06	3470	ADLMGYIPLVGAPLG	HCV Core 131	79	79
	1283.07	3471	GVRVLEDGVNYATGN	HCV Core 154	86	86
	1283.08	3472	GVNYATGNLPGCSFS	HCV Core 161	79	86
	1283.09	3473	GCSFSIFLLALLSCL	HCV Core 171	86	100
	1283.10	3474	GHRMAWDMMMNWSPT	HCV E1 315	86	86
	1283.11	3475	CGPVYCFTPSPVVVG	HCV NS1/E2 506	93	93
	1283.12	3476	VYCFTSPSPVVGTTD	HCV NS1/E2 509	93	93
	1283.13	3477	GNWFGCTWMNSTGFT	HCV NS1/E2 550	79	86
	1283.14	3478	FTTLPALSTGLIHLH	HCV NS1/E2 684	79	86
	1283.17	3479	DLVYLVTRHADVIPVR	HCV NS3 1134	79	79
	1283.18	3480	RAAVCTRGVAKAVDF	HCV NS3 1186	79	79
	1283.20	3481	AQGYKVLVLPNSVAA	HCV NS3 1251	79	100
	1283.21	3482	GYKVLVLPNSVAATL	HCV NS3 1253	100	100
	1283.22	3483	VLVLPNSVAATLGFG	HCV NS3 1256	100	100
	1283.23	3484	GTVLDQAETAGARLV	HCV NS3 1335	86	86
	1283.24	3485	GARLVVLTATPPGS	HCV NS3 1345	79	86
	1283.25	3486	GRHLIFCHSKKCKDE	HCV NS3 1393	100	100
	1283.27	3487	DSVIDCNTCTVTQIVD	HCV NS3 1454	86	86
	1283.28	3488	TVDFSLDPTFTIETT	HCV NS3 1466	79	100
	1283.30	3489	FTGLTHIDAHFLSQT	HCV NS3 1567	93	93
	1283.31	3490	YLVAYQATVCARAQA	HCV NS3 1591	79	93
	1283.32	3491	KPTLHGPTPLLYRLG	HCV NS4 1620	79	79
	1283.33	3492	LEVVTSTWVLVGGVL	HCV NS4 1658	86	86
	1283.34	3493	TWVLVGGVLAALAAAY	HCV NS4 1664	86	86
	1283.35	3494	AEQFKQKALGLLQTA	HCV NS4 1730	86	86
	1283.40	3495	PAILSPGALVVGVCVA	HCV NS4 1889	79	93
	1283.41	3496	GALVVGVCVAAILRR	HCV NS4 1895	79	79
	1283.42	3497	CAAILRRHVGPGEA	HCV NS4 1903	79	79
	1283.43	3498	AVQWMNRLIAFASRG	HCV NS4 1917	100	100
	1283.44	3499	MNRLIAFASRGNHVS	HCV NS4 1921	86	100
	1283.48	3500	ANLLWRQEMGGNITR	HCV NS5 2238	86	86
	1283.49	3501	RQEMGGNITRVESEN	HCV NS5 2243	86	86
	1283.52	3502	ARLIVFPDLGVRVCE	HCV NS5 2610	79	79
	1283.53	3503	FDDLGVVCEKMAVLY	HCV NS5 2615	79	100
	1283.54	3504	GVRVCEKMAVLYDVVS	HCV NS5 2619	79	100
	1283.56	3505	QPEYDLELITSCSSN	HCV NS5 2808	79	93
	1283.57	3506	LELITSCSSNVSVAH	HCV NS5 2813	79	100
	1283.58	3507	PTLWARMILMTHFFS	HCV NS5 2870	79	86
	1283.59	3508	LHGLSAFSLHSYSPG	HCV NS5 2919	79	79
	1283.60	3509	AFSLHSYSPGEINRV	HCV NS5 2924	79	79

Table XXXII. Candidate HCV-derived HTL epitopes

Selection criteria	Peptide	SEQ ID	Sequence	Source	Conservancy	
					Total	Core
B. High algorithm conserved core	1283.15	3510	VVLLFLLADARVCS	HCV NS1/E2 724	29	100
	1283.16	3511	SKGWRL LAPITAYAQ	HCV NS3 1025	29	79
	1283.19	3512	PQTFQVAHLHAPTGS	HCV NS3 1225	43	85
	1283.26	3513	DVVVVATDALMTGYT	HCV NS3 1436	43	79
	1283.29	3514	WESVFTGLTHIDAHF	HCV NS3 1563	43	92
	1283.45	3515	LTSMLTDP SHITAET	HCV NS5 2176	57	100
	1283.46	3516	ASQLSAPSLKATCTT	HCV NS5 2208	50	79
	1283.47	3517	DADLIEANLLWRQEM	HCV NS5 2232	50	85
	1283.50	3518	SYTWTGALITPCAAE	HCV NS5 2456	64	79
	1283.51	3519	TTIMAKNEVFCVQPE	HCV NS5 2589	64	85
	1283.55	3519	GSSYGFQYSPGQRVE	HCV NS5 2641	71	79
C. Collaborator	1283.61	3521	ASCLRKLGVPLRVW	HCV NS5 2939	50	85
	F098.03	3522	AAYAAQGYKVLVLPNSVAAT	HCV NS3 1242-1261	71	100
	F098.04	3523	GYKVLVLPNSVAATLGFGAY	HCV NS3 1248-1267	100	
	F098.05	3524	GYKVLVLPNSVAAT	HCV NS3 1248-1261	100	
	F134.01	3525	RRPQDVKFPGGGQIVGGVY	HCV Core 17-35	86	
	F134.02	3526	DVKFPGGGQIVGGVYLLPRR	HCV Core 21-40	86	
	F134.03	3527	GYKVLVLPNSVAATLGFGAY	HCV NS3 1253-1272	100	
	F134.04	3528	TLHGPTPLLYRLGAVQNEIT	HCV NS4 1622-1641		79
	F134.05	3529	NFISGIQYLAGLSTLPGNPA	HCV NS4 1772-1791	100	
	F134.06	3530	LLFNILGGWVAAQLAAPGAA	HCV NS4 1812-1831		86
	F134.07	3531	GPGEGAVQWMNRLIAFASRG	HCV NS4 1912-1931	86	100
	F134.08	3532	GEGAVQWMNRLIAFASRGNHV	HCV NS4 1914-1934	100	
	Pape 21	3533	AIPLEVIKGRHLIFCHSKR	HCV NS3 1379-1398	21	100
	Pape 22	3534	GRHLIFCHSKRKCDLATKL	HCV NS3 1388-1407		100
	Pape 29	3535	SVIDCNTCVTQTVDFSLDPT	HCV NS3 1450-1469	86	
D. DR3 motif	35.0102	3536	GVRVLEDGVNYATGN	HCV 154	86	86
	35.0103	3537	SAMYVGDLGSGSVFLV	HCV 273	57	86
	35.0104	3538	GHRMAWDMMMNWSPT	HCV 315	86	86
	35.0105	3539	SDLYLVRHADVIPV	HCV 1133	79	86
	35.0106	3540	VVVVATDALMTGYTG	HCV 1437	42	86
	35.0107	3541	TVDFSLDPTFTIETT	HCV 1466	79	100
	35.0108	3542	DSSVLCECYDAGCAW	HCV 1518	71	93
	35.0109	3543	GLPVCQDHLEFWESV	HCV 1552	42	86
	35.0110	3544	GMQLAEQFKQKALGL	HCV 1726	57	86
	35.0111	3545	PTHYVPESDAAARVT	HCV 1936	86	86
	35.0112	3546	GSQLPCEPEPDVAVL	HCV 2162	64	86
	35.0113	3547	LTSMLTDP SHITAET	HCV 2176	57	100
	35.0114	3548	MPPLEGEPPDPLSD	HCV 2401	79	100
	35.0115	3549	QPEYDLELITSCSSN	HCV 2808	79	93
	1283.25	3550	GRHLIFCHSKKKCDE	HCV NS3 1393-1407		

Table XXXIV. HLA-DR binding capacity of target derived peptides: DR-supermotif and algorithm positive peptides.

Peptide	SEQ ID:	Sequence	Source	Binding capacity (IC50 nM)											DR alleles	
				DR1	DR2w2B1	DR2w2B2	DR4w4	DR4w15	DR3w11	DR6w19	DR7	DR8w2	DR9	IAb	bound	
3551		AAVAAQGYKVLVLPNSVAATLQFGAY	HCV NS3 1242-1267													
1283.21	3552	GYKVLVLPNSVAATL	HCV NS3 1253	4.5	350	-	5.2	567	143	5.1	89	288	54	175	9	
1283.20	3553	AQGYKVLVLPNSVAA	HCV NS3 1251	6.0	650	-	7.9	224	74	5.9	833	175	375	298	9	
F98.03	3554	AAVAAQGYKVLVLPNSVAAT	HCV NS3 1242	2.9	48	483	18	1234	103	11	96	60	240		9	
F98.05	3555	GYKVLVLPNSVAAT	HCV NS3 1248-1261	1.4	39	3695	7.8	141	75	3.5	126	21	266		9	
F98.04	3556	GYKVLVLPNSVAATLQFGAY	HCV NS3 1248-1267	3.5	42	8154	9.7	1500	240	4.1	23	80	20		8	
3557		GEGAVQWMNRLIAFASRGNHVS	HCV NS4 1914-1935													
1283.44	3558	MNRLIAFASRGNHVS	HCV NS4 1921	66	4.8	1538	6329	585	45	7.3	227	102	313	147	8	
FI34.08	3559	GEGAVQWMNRLIAFASRGNHV	HCV NS4 1914	3.2		182	361		345		221	158	6818		6	
1283.16	3560	SKGWRLLAIPITAYAQ	HCV NS3 1025	0.36	125	23	24	152	4.8	-	962	54	1190	384	8	
1283.55	3561	GSSYGFGQSPGQRVE	HCV NS5 2641	11	-	667	417	745	20000	19	156	-	68	571	7	
1283.61	3562	ASCLRKLGVPPLRVW	HCV NS5 2939	5.0	16	217	6250	78	645	2500	862	671	8621	-	7	
FI34.05	3563	NFISGIQYLAGLSTLPNPA	HCV NS4 1772	10		606	84		29			70	441		6	

Shading indicates IC50 > 1 µM.

A dash (-) indicates IC50 > 20 µM.

Table XXXV. HLA-DR binding capacity of 3 DR3 motif-containing peptides

Peptide	Seq #	Sequence	Source	DR3 binding* (IC50 nM)
35.0106	3564	VVVVATDALMTGYTG	HCV 1437	427
35.0107	3565	TVDFSLDPTFTIETT	HCV 1466	235
1283.25	3566	GRHLIFCHSKKKCDE	HCV NS3 1393	ND

Table XXXVIa: HCV-derived CTL epitope candidates

Peptide	Molecule	1st Position	Seq ID	Sequence	Consv.	Selection criteria
1073.05	NS4	1812	3567	LLFNILGGWV	85	A2-supertype
1090.18	NS1/E2	728	3568	FLLADARV	92	A2-supertype
1013.02	NS4	1590	3569	YLVAYQATV	85	A2-supertype
1090.22	NS5	2611	3570	RLVFPDLGV	79	A2-supertype
1013.1002	CORE	132	3571	DLMGYPLV	79	A2-supertype
24.0073	NS4	1920	3572	WMNRLIAFA	100	A2-supertype
24.0075	NS4	1666	3573	VLVGGVLAA	85	A2-supertype
1174.08	NS4	1769	3574	HMWNFISGI	92	A2-supertype
1073.06	NS4	1851	3575	ILAGYGAGV	79	A2-supertype
1073.07	CORE	35	3576	YLLPRRGPR	92	A2-supertype
24.0071	NS1/E2	726	3577	LLFLLADA	100	A2-supertype
1.0119	LORF	1131	3578	YLVTRHADV	85	A2-supertype
1.0952	CORE	51	3579	KTSESRQPR	92	A3-supertype
1073.11	CORE	43	3580	RLGVRATRK	79	A3-supertype
1.0955	ENV1	290	3581	QLFTFSRR	79	A3-supertype
1073.13	NS1/E2	632	3582	RMVVGVEHR	100	A3-supertype
1.0123	NS3	1396	3583	LIFCHSKKK	100	A3-supertype
1073.10	NS4	1863	3584	GVAGALVAFK	85	A3-supertype
24.0090	NS4	1864	3585	VAGALVAFK	85	A3-supertype
24.0086	NS3	1262	3586	TLGFGAYMSK	85	A3-supertype
F104.01	NS5	3003	3587	VGYLLPNR	79	A31
1145.12	Core	169	3588	LPGCSFSIF	92	B7-supertype
29.0035	NS3	1378	3589	IPFYGKAI	92	B7-supertype
13.0019	NS5	2922	3590	LSAFSLHSY	79	A1
1069.62	NS3	1128	3591	CTCGSSDLY	79	A1
24.0092	NS4	1765	3592	FWAKHMMWNF	85	A24

Table XXXVIIb. HCV-derived HTL epitope candidates

Region	Peptide	Motif ¹	Seq ID	Sequence
HCV NS3 1025-1039	1283.16	DR	3593	SKGWRLLAPITAYAQ
HCV NS3 1242-1267	F98.03	DR	3594	AAYAAQGYKVLNPSVAAT
HCV NS3 1393-1407	1283.25	DR3	3595	GRHLIFCHSKKCKDE
HCV NS3 1437-1451	35.0106	DR3	3596	VVVVATDALMTGYTG
HCV NS3 1466-1480	35.0107	DR3	3597	TVDFSLDPTFTIETT
HCV NS4 1772-1790	F134.05	DR	3598	NFISGIQYLAGLSTLPGNPA
HCV NS4 1914-1935	F134.08	DR	3599	GEGAVQWMNRIAFASRGNHV
HCV NS5 2641-2655	1283.55	DR	3600	GSSYGFGQYSPGQERVE
HCV NS5 2939-2953	1283.61	DR	3601	ASCLRKLGVPPLRVW

1. Peptides identified on the basis of either the DR P1-P6 supermotif or by use of the DR1-4-7 algorithms are indicated by 'DR'. Peptides identified using the DR3 motif are indicated by 'DR3'.

EXHIBIT

B

(Appl. No.: 09/357,737)

09/357,737 INDUCING CELLULAR IMMUNE RESPONSES TO HEPATITIS VIRUS 10-19-
USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS 2007::14:08:12

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07-05-2007	WFEE	Fee Worksheet (PTO-06)	PROSECUTION	1
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05-15-2006	XT/	Extension of Time	PROSECUTION	1
05-15-2006	LET.	Miscellaneous Incoming Letter	PROSECUTION	3
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11-15-2005	SRFW	Search information including classification, databases and other search related notes	PROSECUTION	1
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08-29-2005	A...	Amendment - After Non-Final Rejection	PROSECUTION	1
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08-29-2005	FOR	Foreign Reference	PRIOR ART	110
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08-29-2005	NPL	NPL Documents	PRIOR ART	3
08-29-2005	NPL	NPL Documents	PRIOR ART	41
08-29-2005	136A	Authorization for Extension of Time all replies	PROSECUTION	2
08-29-2005	WFEE	Fee Worksheet (PTO-06)	PROSECUTION	2
03-07-2005	EBCC.AD	Notice of Change of Address placed in File Wrapper due to EBC Customer Number	PROSECUTION	1

		update		
02-28-2005	CTNF	Non-Final Rejection	PROSECUTION	8
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10-16-2002	XT/	Extension of Time	PROSECUTION	1
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05-16-2002	CLM	Claims	PROSECUTION	6
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05-16-2002	LET.	Miscellaneous Incoming Letter	PROSECUTION	3
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04-24-2002	CTMS	Miscellaneous Action with SSP	PROSECUTION	1
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03-26-2002	LET.	Miscellaneous Incoming Letter	PROSECUTION	3

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11-20-2000	SPEC	Specification	PROSECUTION	2
11-20-2000	XT/	Extension of Time	PROSECUTION	1
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08-14-2000	PET.	Petition Entered	PROSECUTION	2
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04-10-2000	CLM	Claims	PROSECUTION	4
04-10-2000	REM	Applicant Arguments/Remarks Made in an Amendment	PROSECUTION	2
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07-20-1999	FWCLM	Index of Claims	PROSECUTION	1

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